

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:02:36 ; Search time 230 Seconds

(without alignments) 1208.601 Million cell updates/sec

Title: US-10-689-461-2

Sequence: 1 MEVMPMEGSGMGRRTTSF.....QELSNPLATLIRPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	96.7	420	1	GSK3B_HUMAN
2	2013	96.7	420	1	GSK3B_MOUSE
3	2013	96.7	420	1	GSK3B_HUMAN
4	2013	96.7	420	1	GSK3B_MOUSE
5	2010	96.6	420	1	GSK3B_RAT
6	2006	96.4	420	2	OSYJC2_SPECTI
7	1959	94.1	421	2	OSYJC2_SPECTI
8	1959	94.1	421	2	OSYJC2_SPECTI
9	1931	92.8	420	2	OSYJC2_SPECTI
10	1923	92.4	420	2	OSYJC2_SPECTI
11	1793.5	86.2	440	2	OSYJC2_SPECTI
12	1704.5	81.9	440	2	OSYJC2_SPECTI
13	1669.5	80.2	435	2	OSYJC2_SPECTI
14	1669.5	80.1	435	2	OSYJC2_SPECTI
15	1632	78.4	414	2	OSYJC2_SPECTI
16	1614	77.6	414	2	OSYJC2_SPECTI
17	1609	77.3	483	1	GSK3A_HUMAN
18	1607	77.2	483	1	GSK3A_HUMAN
19	1606	77.2	399	2	QASSG6_TERNING
20	1594	76.6	388	2	QASSG6_TERNING
21	1565	75.2	363	3	QASSG6_TERNING
22	1542.5	74.1	1067	1	SGG_DROME
23	1495.5	71.9	443	2	QASSG6_TERNING
24	1485	71.4	442	2	QASSG6_TERNING
25	1443	69.3	431	2	QASSG6_TERNING
26	1343.5	64.6	362	2	QASSG6_TERNING
27	1342.5	64.5	362	2	QASSG6_TERNING
28	1341.5	64.5	359	2	QASSG6_TERNING
29	1305.5	62.7	501	1	GSK3H_DROME
30	1302	62.6	402	2	QASSG6_TERNING
31	1296	62.3	409	2	QASSG6_TERNING

32	1294	62.2	423	2	QASSG6_TERNING
33	1289.5	62.0	398	2	QASSG6_TERNING
34	1289.5	62.0	398	2	QASSG6_TERNING
35	1283	61.7	410	1	KSG5_ARATH
36	1275.5	61.3	471	2	QASSG6_TERNING
37	1273.5	61.2	424	2	QASSG6_TERNING
38	1273.5	61.2	471	2	QASSG6_TERNING
39	1273	61.2	401	2	QASSG6_TERNING
40	1271	61.1	423	2	QASSG6_TERNING
41	1269	61.0	412	2	QASSG6_TERNING
42	1264	60.7	394	2	QASSG6_TERNING
43	1263.5	60.7	424	2	QASSG6_TERNING
44	1262.5	60.7	470	2	QASSG6_TERNING
45	1262	60.6	355	2	QASSG6_TERNING

ALIGNMENTS

RESULT 1

GSK3B_HUMAN

AC P49841; OSBMH3; Q9UL47;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta).

GN Name=GSK3B;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

[1]

NUCLEOTIDE SEQUENCE (ISOFORM 1).

RA MEDLINE=95071278; PubMed=7980435;

RT Stambolic V., Woodgett J.R.;

RT "Mitogen inactivation of glycogen synthase kinase-3 beta in intact cells via serine 9 phosphorylation.";

RL Biochem. J. 303:701-704(1994).

[2]

NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORMS 1 AND 2).

RP TISSUE=Eye, and Placenta;

RC MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;

RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,

RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosack S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schermer A., Schin J.E., Jones S.J.W., Merra M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

NUCLEOTIDE SEQUENCE OF 185-202.

RA MEDLINE=99455114; PubMed=10523816; DOI=10.1038/sj.mp.4000538;

RA Rhoads A.R., Karkera J.D., Decker-Wadleigh S.D.,

RT "Radiation hybrid mapping of genes in the lithium-sensitive wnt signaling pathway.";

RL Mol. Psychiatry 4:437-442(1999).

[4]

NUCLEOTIDE SEQUENCE OF 1-28.

RX MEDLINE=59411672; PubMed=10486203; DOI=10.1006/geno.1999.5875;
 RA Lau K.F., Miller C.C.U., Anderson B.H., Shaw P.C.;
 RT "Molecular cloning and characterization of the human glycogen synthase
 RL kinase-3beta promoter."; *Genomics* 60:121-128(1999).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=99409636; PubMed=9736715; DOI=10.1073/pnas.95.19.11211;
 RA Delcienne M., Tan C., Gray V., Rue L., Woodgett J.R., Dedhar S.;
 RT "Phosphoinositide-3-OH kinase-dependent regulation of glycogen
 RL synthase kinase 3 and protein kinase B/AKT by the integrin-linked
 RL kinase."; *Proc. Natl. Acad. Sci. U.S.A.* 95:11211-11216(1998).
 RN [6]
 RP INTERACTION WITH NIN.
 RX MEDLINE=20461863; PubMed=11004522; DOI=10.1016/S0167-4781(00)00127-5;
 RA Hong Y.-R., Chen C.-H., Chang J.-H., Wang S.-K., Sy W.-D., Chou C.-K.,
 RL Hwang S.-L.;
 RN "Cloning and characterization of a novel human ninein protein that
 RT interacts with the glycogen synthase kinase 3beta."; *Biochim. Biophys. Acta* 1492:513-516(2000).
 RN [7]
 RP PHOSPHORYLATION SITE THR-390.
 RX PubMed=15302935; DOI=10.1073/pnas.0404720101;
 RA Beausoleil S.A., Jedrychowski M., Schwartz D., Elias J.E., Villen J.,
 RL Li J., Comn M.A., Cantley L.C., Gygi S.P.;
 RN "Large-scale characterization of HeLa cell nuclear phosphoproteins."; *Proc. Natl. Acad. Sci. U.S.A.* 101:12130-12135(2004).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 35-366
 RX MEDLINE=21334145; PubMed=11440715; DOI=10.1016/S0092-8674(01)00374-9;
 RA Dajani R., Fraser E., Roe S.M., Young N., Good V., Dale T.C.,
 RL Pearl L.H.;
 RN "Crystal structure of glycogen synthase kinase 3 beta: structural
 RT basis for phosphate-primed substrate specificity and autoinhibition."; *Cell* 105:721-732(2001).
 RL [9]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 27-393 OF PHOSPHORYLATED
 RX GSK3B.
 RA MEDLINE=21605727; PubMed=11738041; DOI=10.1016/S0969-2126(01)00679-7;
 RL Bax B., Carter P.S., Lewis C., Guy A.R., Bridges A., Tanner R.,
 RA Petman G., Mannix C., Culbert A.A., Brown M.U.B., Smith D.G.,
 RL Reith A.D.;
 RN "The structure of phosphorylated GSK-3beta complexed with a peptide,
 RT FRATride, that inhibits beta-catenin phosphorylation."; *Structure* 9:1143-1152(2001).
 RL [10]
 RP FUNCTION: Participates in the Wnt signaling pathway. Implicated in
 CC the hormonal control of several regulatory proteins including
 CC glycogen synthase, MYB and the transcription factor JUN.
 CC Phosphorylates JUN at sites proximal to its DNA-binding domain,
 CC thereby reducing its affinity for DNA.
 CC [11]
 RP CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC [12]
 RP ENZYME REGULATION: Inhibited when phosphorylated by AKT1.
 CC [13]
 RP SUBUNIT: Monomer (By similarity). Interacts with NIN.
 CC [14]
 RP INTERACTION:
 CC Q7Z6N3:UPEF3A; NBEXP=1; IntAct=EBI-373586, EBI-372587;
 CC [15]
 RP ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49841-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49841-2; Sequence=VSP_004790;
 CC Note=No experimental confirmation available;
 CC [16]
 RP TISSUE SPECIFICITY: Expressed in testis, thymus, prostate and
 CC ovary and weakly expressed in lung, brain and kidney.
 CC [17]
 RP PTM: Phosphorylated by AKT1 and ILK1.
 CC [18]
 RP SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
 CC subfamily.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not

CC	removed.	
CC	removed.	
DR	EMBL; L33801; AAA66475.1; -; mRNA.	
DR	EMBL; BC000251; AAH00251.1; -; mRNA.	
DR	EMBL; BC012760; AAH12760.1; -; mRNA.	
DR	EMBL; AF098789; AAC69340.1; -; Genomic DNA.	
DR	EMBL; AF074333; AAD48517.1; -; Genomic DNA.	
DR	PIR; S53324; S53324.	
DR	PDB; 1GNG; X-ray; A/B=27-393.	
DR	PDB; 1H8F; X-ray; A/B=35-386.	
DR	PDB; 1I09; X-ray; A/B=1-420.	
DR	PDB; 1J1B; X-ray; A/B=1-420.	
DR	PDB; 1J1C; X-ray; A/B=1-420.	
DR	PDB; 1O9Y; X-ray; A=35-384.	
DR	PDB; 1PXY; X-ray; A/B=1-420.	
DR	PDB; 1Q3D; X-ray; A/B=2-420.	
DR	PDB; 1Q3W; X-ray; A/B=2-420.	
DR	PDB; 1Q41; X-ray; A/B=2-420.	
DR	PDB; 1Q4L; X-ray; A/B=2-420.	
DR	PDB; 1Q5K; X-ray; A/B=7-420.	
DR	PDB; 1R0E; X-ray; A/B=35-420.	
DR	PDB; 1UV5; X-ray; A=35-384.	
DR	InterPro; IPR008271; Ser_Thr_pkin.AS.	
DR	InterPro; IPR002290; Ser_Thr_pkinase.	
DR	Pfam; PF00069; Pkinase; 1.	
DR	ProDom; PD000001; Prot_kinase; 1.	
DR	SMART; SM00220; S_TKc.1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
KW	3D-structure; Alternative splicing; ATP-binding; kinase;	
KW	Multiple family; Nucleotide-binding; phosphorylation;	
KW	Serine/threonine-protein kinase; Transferase; Wnt signaling pathway	
FT	DOMAIN	56 340
FT	NBP BIND	62 70
FT	ACT_SITE	181 181
FT	BINDING	85 85
FT	MOD_RES	9 9
FT	MOD_RES	216 216
FT	MOD_RES	390 390
FT	VARSP	303 303
FT	MUTAGEN	9 9
FT	CONFLICT	28 28
FT	CONFLICT	350 350
FT	TUNN	30 30
FT	TUNN	32 33
FT	TUNN	36 44
FT	STRAND	52 63
FT	STRAND	68 75
FT	STRAND	81 90
FT	TUNN	91 92
FT	HELIIX	96 103
FT	TUNN	107 108
FT	STRAND	109 109
FT	STRAND	112 119
FT	STRAND	125 133
FT	STRAND	138 138
FT	HELIIX	139 148
FT	HELIIX	149 150
FT	HELIIX	155 174
FT	TUNN	175 176
FT	STRAND	177 178

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FT  HELIX      184   186
FT  STRAND     187   189

Query Match
Best Local Similarity 96.7%; Score 2013; DB 1; Length 420;
Pred. No. 4.9e-13;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11 MSGRRPTTSFASBSCVPVOQPSAFGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYTDTK 70
DB  1 MSGRRPTTSFASBSCVPVOQPSAFGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYTDTK 60
QY  71 VIGGSGFVGVOYQAKLCDSGELVAIKVLODKRFKREIQIMRKLDHCNIVLRKYFYSYG 130
DB  61 VIGGSGFVGVOYQAKLCDSGELVAIKVLODKRFKREIQIMRKLDHCNIVLRKYFYSYG 120
QY  131 EKKDEVYLVLDVYPPETVYRVARHYSRAKOTLPVTVYKLVYMYQLFRSLAYIHSPGICHR 190
DB  121 EKKDEVYLVLDVYPPETVYRVARHYSRAKOTLPVTVYKLVYMYQLFRSLAYIHSPGICHR 180
QY  191 DIKQNLILDDPTAVLKLCDPFSAKQIVRGEPNYSYICSRYYRABELIFGATDYSSIDV 250
DB  181 DIKQNLILDDPTAVLKLCDPFSAKQIVRGEPNYSYICSRYYRABELIFGATDYSSIDV 240
QY  251 MSAGCVLAEILGQPIFGDSGVOLVRIKVLGPTREQIREMNPNTPEKPIKAKP 310
DB  241 MSAGCVLAEILGQPIFGDSGVOLVRIKVLGPTREQIREMNPNTPEKPIKAKP 300
QY  311 WTKVFRPTPEPAIALCSRLLEYTPPALTPLEACAHSPFDELADPNVKGPRDTPALF 370
DB  301 WTKVFRPTPEPAIALCSRLLEYTPPALTPLEACAHSPFDELADPNVKGPRDTPALF 360
QY  371 NFTQELSSNPPLATILIPPHARI 394
DB  361 NFTQELSSNPPLATILIPPHARI 384

RESULT 2
GSK3B_MOUSE
ID  GSK3B_MOUSE STANDARD; PRT; 420 AA.
AC  Q9WV60;
DT  16-OCT-2001 (Rel. 40; Created)
DT  16-OCT-2001 (Rel. 40; Last sequence update)
DT  13-SEP-2005 (Rel. 48; Last annotation update)
DE  Glycogen synthase kinase-3 beta (BC 2.7.1.37) (GSK-3 beta).
GN  Name=Gsk3b;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridea; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  Tissue=Testis;
RA  Salameh W.A., Guo T.B., Chan K.C., Mitchell A.P.;
RT  "Testicular expression and hormonal control of glycogen synthase
RL  kinase 3, a homologue of yeast RIM1.",
RL  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC  STRAIN=Czech 11, and FVB/N; TISSUE=Mammary gland;
RX  MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Ditchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinck P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.H.,
RA  Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA  Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC  -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in
CC  the hormonal control of several regulatory proteins including
CC  glycogen synthase, MYB and the transcription factor JUN (By
CC  similarity).
CC  -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC  -1- SUBUNIT: Monomer. Interacts with NIN (By similarity).
CC  -1- PTM: Phosphorylation on Tyr-216 is necessary for the activity (By
CC  similarity).
CC  -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3
CC  subfamily.
-----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
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DR  EMBL; AF156099; AA039258.2; -; mRNA.
DR  EMBL; BC006936; AA06936.1; -; mRNA.
DR  EMBL; BC060743; AA060743.1; -; mRNA.
DR  HSSP; P49841; 1GNG.
DR  SMR; Q9WV60; 23-386.
DR  Ensembl; ENSMUSG00000022812; Mus musculus.
DR  MGI; MGI:1861437; Gsk3b.
DR  GO; GO:0005829; C:cytosol; IDA.
DR  GO; GO:0005634; C:nucleus; IDA.
DR  GO; GO:0008013; F:beta-catenin binding; IPI.
DR  GO; GO:0050321; F:tau-protein kinase activity; IDA.
DR  GO; GO:0006916; P:anti-apoptosis; IMP.
DR  GO; GO:0008283; P:cell proliferation; TAS.
DR  GO; GO:0045444; P:fat cell differentiation; IDA.
DR  GO; GO:0009887; P:organogenesis; IMP.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR  GO; GO:0006611; P:protein-nucleus export; IDA.
DR  GO; GO:0000320; P:entry into mitotic cell cycle; IDA.
DR  GO; GO:0006950; P:response to stress; IDA.
DR  GO; GO:0006950; P:response to stress; IDA.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR008271; Ser_thr_pkin_AS.
DR  InterPro; IPR002290; Ser_thr_pkinase.
DR  Pfam; PF00069; Pkinase; I.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00220; S_TKc; 1.
DR  PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR  PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW  ATP-binding; Kinase; Multigene family; Nucleotide-binding;
KW  Phosphorylation; Serine/threonine-protein kinase; Transferase;
KW  Wnt signaling pathway.
FT  DOMAIN 56 340 Protein kinase.
FT  NP BIND 62 70 ATP (By similarity).
FT  ACT SITE 181 181 Proton acceptor (By similarity).
FT  BINDING 85 85 ATP (By similarity)
FT  MOD_RES 9 9 Phosphoserine (by PKA/AKT1) (By
FT  MOD_RES 9 9 similarity).
FT  MOD_RES 216 216 Phosphotyrosine (By similarity).
SQ  SEQUENCE 420 AA; 46710 MW; 200C3FD1B3854883 CRC64;

Query Match
Best Local Similarity 96.7%; Score 2013; DB 1; Length 420;
Pred. No. 4.9e-13;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11 MSGRRPTTSFASBSCVPVOQPSAFGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYTDTK 70
DB  1 MSGRRPTTSFASBSCVPVOQPSAFGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYTDTK 60

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Qy 71 VINGSGFVGYOAKLDCSGLVAIKKVLQDKRFKQRELOIMRLDHCNIVRLAYFFYS5G 130
Db 61 VINGSGFVGYOAKLDCSGLVAIKKVLQDKRFKQRELOIMRLDHCNIVRLAYFFYS5G 120
Qy 131 EKKDEVYLNVLVDYVETVYRVARHYSRAKQTLPIVIYVKLYMYQLFSLAYHSFGICHR 190
Db 121 EKKDEVYLNVLVDYVETVYRVARHYSRAKQTLPIVIYVKLYMYQLFSLAYHSFGICHR 180
Qy 191 DIRQNLLDPDPAVLKLCFSGAKOLVRGEPNVSYICSRYYRABELIFGATDYSIDV 250
Db 181 DIRQNLLDPDPAVLKLCFSGAKOLVRGEPNVSYICSRYYRABELIFGATDYSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVOLVEIIVKLTGPTREQIREMNPYTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVOLVEIIVKLTGPTREQIREMNPYTEKFPQIKAMP 300
Qy 311 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPVVKHNGRDPALF 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPVVKHNGRDPALF 360
Qy 371 NPTTQELSSNPPLATLILIPPHARI 394
Db 361 NPTTQELSSNPPLATLILIPPHARI 384

RESULT 3
06F127 HUMAN
ID 06F127_HUMAN PRELIMINARY; PRT; 420 AA.
AC 06F127;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE GSK3B protein.
GN Name=GSK3B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kerrang K., Schacten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; CR536510; CA638748.1; -; mRNA.
DR SMR; Q6F127; 23-386.
DR Ensembl; ENSG00000082701; Homo sapiens.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 4ACC24D00CDBB9C3 CRC64;

Query Match 96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 4.9e-11;
Matches 383; Conservative 0; Mismatch 1; Indels 0; Gaps 0;
Qy 11 MSGRPRTTSPAECKPVQPSAFGSMKVSRLDKDSKVTTVATPGQDPDRQEVSYDTK 70
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Db 1 MSGRPRTTSPAECKPVQPSAFGSMKVSRLDKDSKVTTVATPGQDPDRQEVSYDTK 60
Qy 71 VINGSGFVGYOAKLDCSGLVAIKKVLQDKRFKQRELOIMRLDHCNIVRLAYFFYS5G 130
Db 61 VINGSGFVGYOAKLDCSGLVAIKKVLQDKRFKQRELOIMRLDHCNIVRLAYFFYS5G 120
Qy 131 EKKDEVYLNVLVDYVETVYRVARHYSRAKQTLPIVIYVKLYMYQLFSLAYHSFGICHR 190
Db 121 EKKDEVYLNVLVDYVETVYRVARHYSRAKQTLPIVIYVKLYMYQLFSLAYHSFGICHR 180
Qy 191 DIRQNLLDPDPAVLKLCFSGAKOLVRGEPNVSYICSRYYRABELIFGATDYSIDV 250
Db 181 DIRQNLLDPDPAVLKLCFSGAKOLVRGEPNVSYICSRYYRABELIFGATDYSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSGVOLVEIIVKLTGPTREQIREMNPYTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFGDSGVOLVEIIVKLTGPTREQIREMNPYTEKFPQIKAMP 300
Qy 311 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPVVKHNGRDPALF 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPPARLTPLEACAHSPFDELDPVVKHNGRDPALF 360
Qy 371 NPTTQELSSNPPLATLILIPPHARI 394
Db 361 NPTTQELSSNPPLATLILIPPHARI 384

RESULT 4
Q5KU03 MOUSE
ID Q5KU03_MOUSE PRELIMINARY; PRT; 420 AA.
AC Q5KU03;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE Glycogen synthase kinase 3b, last annotation update)
DE Glycogen synthase kinase 3 beta/tau protein kinase I.
GN Name=Gsk3b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sano Y., Nakano A., Hirai K., Ohta S., Yanagisawa M., Sato S.,
RA Tanori K.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB066114; BAB8627.1; -; mRNA.
DR SMR; Q5KU03; 23-386.
DR Ensembl; ENSMUSG0000002812; Mus musculus.
DR MGI; MGI:1861437; Gsk3b.
DR GO; GO:0005829; C:cytosol; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0008013; F:beta-casein binding; IPI.
DR GO; GO:0005031; F:tau-protein kinase activity; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IMP.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0045444; P:fat cell differentiation; IEA.
DR GO; GO:0009887; P:organogenesis; IMP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006611; P:protein-nucleus export; IEA.
DR GO; GO:0000320; P:pre-entry into mitotic cell cycle; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
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DR SMART: SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 420 AA; 46710 MW; 200C3FD1B38B8683 CRC64;

Query Match 96.7%; Score 2013; DB 2; Length 420;
 Best Local Similarity 99.7%; Pred. No. 4.9e-131;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFGSMKVSRLDGSKVTTVATPGQGPDRPOEVSYTDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFGSMKVSRLDGSKVTTVATPGQGPDRPOEVSYTDTK 60

QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLODRKFKRREIQMRKLDHCNIVRLRYFFYSSG 130
 DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLODRKFKRREIQMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKQDEVYLVLDVYVETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKQDEVYLVLDVYVETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 180

QY 191 DIKQNLILDPDTAVLKLCDFGSAQQLYRGEPNVSYSRYTRABELFGATDYTSIDV 250
 DB 181 DIKQNLILDPDTAVLKLCDFGSAQQLYRGEPNVSYSRYTRABELFGATDYTSIDV 240

QY 251 MSAGCVLAEILLGQIFPGDSDVDQVLEIKVIGTPTRERQIREMKNPNTFEKFOIKAMP 310
 DB 241 MSAGCVLAEILLGQIFPGDSDVDQVLEIKVIGTPTRERQIREMKNPNTFEKFOIKAMP 300

QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLLEACAHSPFDELNDPNYKHPGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLLEACAHSPFDELNDPNYKHPGRDTPALF 360

QY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 5
 GSK3B_RAT STANDARD; PRT; 420 AA.
 ID GSK3B_RAT
 AC P18266;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glycogen synthase kinase-3 beta (EC 2.7.1.37) (GSK-3 beta) (Factor A) (FA).
 DB Name=Gsk3b;
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=90316097; PubMed=2164470;
 RA Woodgett J.R.;
 RT "Molecular cloning and expression of glycogen synthase kinase-3/factor A";
 RL EMBO J. 9:2431-2438(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=93307488; PubMed=7686508; DOI=10.1016/0014-5793(93)81066-9;
 RA Ishiguro K., Shiratauchi A., Sato S., Omori A., Arioka M., Kobayashi S., Uchida T., Imahori K.;
 RT "Glycogen synthase kinase 3 beta is identical to tau protein kinase I generating several epitopes of paired helical filaments";
 RL FEBS Lett. 325:167-172(1993).

RN [3]
 RP PHOSPHORYLATION SITE TYR-216.
 RX MEDLINE=93178457; PubMed=8382613;
 RA Hughes K., Nikolakaki B., Pyle S.E., Totty N.F., Woodgett J.R.;
 RT "Modulation of the glycogen synthase kinase-3 family by tyrosine phosphorylation";
 RL EMBO J. 12:803-808(1993).
 CC -1- FUNCTION: Participates in the Wnt signaling pathway. Implicated in the hormonal control of several regulatory proteins including glycogen synthase, MYB and the transcription factor JUN.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Interacts with NIN (By similarity). Monomer.
 CC -1- PM: Phosphorylation of Tyr-216 is necessary for the activity.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. GSK-3 subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; X53428; CAA37519.1; -; mRNA.
 CC EMBL; X73653; CAA52020.1; -; mRNA.
 CC PIR; S14708; TYRKB.
 CC HSSP; P49841; 1109.
 DR SMR; P18266; 23-386.
 DR Ensembl; ENSRNOC000002833; Rattus norvegicus.
 DR RGD; 70982; Gsk3b.
 DR GO; GO:0004696; F:glycogen synthase kinase 3 activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0030010; P:establishment of cell polarity; IDA.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR GO; GO:0045892; P:negative regulation of transcription, DNA-d. . .; IDA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Multigene family; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase; Wnt signaling pathway.
 KW Domain
 FT NP_BIND 56 340 Protein kinase.
 FT ACT_SITE 62 70 ATP (By similarity).
 FT BINDING 85 85 Proton acceptor (By similarity).
 FT MOD_RES 9 9 Phosphoserine (by PKB/AKT1) (By similarity).
 FT MOD_RES 216 216 Phosphotyrosine.
 FT MUTAGEN 216 216 Y->F: Loss of phosphorylation.
 FT CONFLICT 240 240 M -> V (in Ref. 2).
 SQ SEQUENCE 420 AA; 46742 MW; 2F473FCAB894398 CRC64;

Query Match 96.6%; Score 2010; DB 1; Length 420;
 Best Local Similarity 99.5%; Pred. No. 7.9e-131;
 Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFGSMKVSRLDGSKVTTVATPGQGPDRPOEVSYTDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFGSMKVSRLDGSKVTTVATPGQGPDRPOEVSYTDTK 60

QY 71 VINGSGFVGVYQAKLCDSGELVAIKVLODRKFKRREIQMRKLDHCNIVRLRYFFYSSG 130
 DB 61 VINGSGFVGVYQAKLCDSGELVAIKVLODRKFKRREIQMRKLDHCNIVRLRYFFYSSG 120

QY 131 EKQDEVYLVLDVYVETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKQDEVYLVLDVYVETVYVVAHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSGICHR 180

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Qy 191 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDVTSSIDV 250
Db 181 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDVTSSIDM 240
Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQI REMNPVTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQI REMNPVTEKFPQIKAMP 300
Qy 311 WTKVFRPRTPPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELRDPVAKHPNGRDTPALF 370
Db 301 WTKVFRPRTPPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELRDPVAKHPNGRDTPALF 360
Qy 371 NFTQELSSNPPLATILIPPHARI 394
Db 361 NFTQELSSNPPLATILIPPHARI 384

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RESULT 6

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Q5YJC2 SPECI PRELIMINARY; PRT; 420 AA.
ID 05YJC2
AC 05YJC2
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Glycogen synthase kinase 3 beta.
OS Sperophilus citellus (European musk) (Citellus citellus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Sciuridae; Sciurinae; Spermophilus.
OX NCBI_TaxID=9997;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA "Stefeler J.T., Strijkstra A.M.;
RT "Molecular cloning of Spermophilus citellus glycogen synthase kinase 3
beta."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AY392021; AAC59774.1; -, mRNA.
DR SMR: Q5YJC2; 23-386.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot. kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 420 AA; 46744 MW; 3F5243CA7D9EA549 CRC64;

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Query Match 96.4%; Score 2006; DB 2; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.5e-10;
Matches 382; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 11 MSGRPRTTSFAESCKPVQGPSAFSGMKVSRDKGSKVTTVATRGQGPDRQEVSYTDK 70
Db 1 MSGRPRTTSFAESCKPVQGPSAFSGMKVSRDKGSKVTTVATRGQGPDRQEVSYTDK 60
Qy 71 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 130
Db 61 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 120
Qy 131 EKQDEVVLNVLVDVPEVTVYVAHYSRAKQTLPIYVLYKLVMYQLFRSLAYHSFGICHR 190

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Db 121 EKQDEVVLNVLVDVPEVTVYVAHYSRAKQTLPIYVLYKLVMYQLFRSLAYHSFGICHR 180
Qy 191 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDVTSSIDV 250
Db 181 DIKQNLDDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDVTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQI REMNPVTEKFPQIKAMP 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQI REMNPVTEKFPQIKAMP 300
Qy 311 WTKVFRPRTPPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELRDPVAKHPNGRDTPALF 370
Db 301 WTKVFRPRTPPEAIALCSRLLEYTPPTARLTPLEACAHSPFDELRDPVAKHPNGRDTPALF 360
Qy 371 NFTQELSSNPPLATILIPPHARI 394
Db 361 NFTQELSSNPPLATILIPPHARI 384

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RESULT 7

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Q9IBD2 BRABE PRELIMINARY; PRT; 421 AA.
ID Q9IBD2
AC Q9IBD2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Glycogen synthase kinase 3 beta.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RX Shimizu T., Yamamaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.;
RT "Cooperative roles of Bcozoxk/Dharma and Nodal-related proteins in the
formation of the dorsal organizer in zebrafish."
RL Mech. Dev. 91:293-303(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AB032265; BAA92442.1; -, mRNA.
DR HSSP: P49841; 1109.
DR SMR: Q9IBD2; 23-386.
DR Ensemble: ENSDARG00000017803; Danio rerio.
DR ZFIN: ZDB-GENE-990714-4; gsk3b.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot. kinase.
DR InterPro: IPR008271; Ser_Thr_Pkin_AS.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot. kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 421 AA; 46856 MW; 2B251B4C66C000EB CRC64;

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Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 2.7e-127;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy 11 MSGRPRTTSFAESCKPVQGPSAFSGMKVSRDKGSKVTTVATRGQGPDRQEVSYTDK 70
Db 1 MSGRPRTTSFAESCKPVQGPSAFSGMKVSRDKGSKVTTVATRGQGPDRQEVSYTDK 60
Qy 71 VINGSGGVVYQAKLCSGSELVAIKVLODKRPNKRELQIMRKLDHCNIVRLRYFFYS 130

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Db 61 VIGNGSFQVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCHIVLRIRFFYS5G 120
Qy 131 EKQDEVYINLVLDVPEYTVVVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 190
Db 121 DKQDEVYINLVLDVPEYTVVVARHYSRAKQTLPMVYKLYMYOLFSLAYIHSFGICHR 180
Qy 191 DIKQNLILDDPTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 250
Db 181 DIKQNLILDDPTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 240
Qy 251 MSAGCVLAELLGQPIFGDGSVDQVLEIIKVLGTPFREQIREMNPNTTEKFPQIKAH 310
Db 241 MSAGCVLAELLGQPIFGDGSVDQVLEIIKVLGTPFREQIREMNPNTTEKFPQIKAH 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKHPNGRDPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKHPNGRDPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHAR 393
Db 361 NFTTOELSSNPPLATILIPPHAR 383
RESULT 8
Q9YH60_BRARE PRELIMINARY; PRT; 421 AA.
AC Q9YH60;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glycogen synthase kinase 3.
GN Name=gsk3b; Synonyms=GSK3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
RT "Differential expression of glycogen synthase kinase 3 genes during zebrafish embryogenesis."; Mech. Dev. 91:387-391(2000).
RL -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
DR EMBL; AJ223502; CAA11420.1; -, mRNA.
DR HSSP; P49841; 1109.
DR SMK; Q9YH60; 23-386.
DR Ensembl; ENSDARG0000017803; Danio rerio.
DR ZFIN; ZDB-GENE-990714-4; gsk3b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 421 AA; 46872 MW; 2B51B4C7B6C00B CRC64;
Query Match 94.1%; Score 1959; DB 2; Length 421;
Best Local Similarity 96.9%; Pred. No. 2.7e-127;
Matches 371; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Qy 11 MSGRRPTTSFASCKPVPQPSAFGSMKVSRLDKSGSKVTTVATPGCGPDRQEVSYTDTK 70

Db 1 MSGRRPTTSFASCKPVPQPSAFGSMKVSRLDKSGSKVTTVATPGCGPDRQEVSYTDTK 60
Qy 71 VIGNGSFQVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCHIVLRIRFFYS5G 130
Db 61 VIGNGSFQVYVQAKLCSGSELVAIKVLODKRFKRELQIMRKLDHCHIVLRIRFFYS5G 120
Qy 131 EKQDEVYINLVLDVPEYTVVVARHYSRAKQTLPIVIYKLYMYOLFSLAYIHSFGICHR 190
Db 121 DKQDEVYINLVLDVPEYTVVVARHYSRAKQTLPMVYKLYMYOLFSLAYIHSFGICHR 180
Qy 191 DIKQNLILDDPTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 250
Db 181 DIKQNLILDDPTAVLKLCDFGSAKQVLRGEPNVSYSRSRYRABELIFGATDYSIDV 240
Qy 251 MSAGCVLAELLGQPIFGDGSVDQVLEIIKVLGTPFREQIREMNPNTTEKFPQIKAH 310
Db 241 MSAGCVLAELLGQPIFGDGSVDQVLEIIKVLGTPFREQIREMNPNTTEKFPQIKAH 300
Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKHPNGRDPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELRDPNVKHPNGRDPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHAR 393
Db 361 NFTTOELSSNPPLATILIPPHAR 383
RESULT 9
Q91757_XENLA PRELIMINARY; PRT; 420 AA.
AC Q91757;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Intracellular kinase.
GN Name=xgsk-3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
CX NCBI_TaxID=8355;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=95237008; PubMed=7720580;
RA Pierce S.B., Kimmel D.;
RT "Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3."; Development 121:755-765(1995).
RL -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; L38492; AAC42224.1; -, mRNA.
DR PIR; I51425; I51425.
DR HSSP; P49841; 1109.
DR SMK; Q91757; 23-386.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 420 AA; 46903 MW; C02280B8A35785D CRC64;
Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 2.3e-125;

Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFGSMKYSRDKGSKTTTVAATPGQDPDRQEVSYDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFGSMKYSRDKGSKTTTVAATPGQDPDRQEVSYDTK 60
 QY 71 VINGSGFGVYVQAKLCSGSELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 130
 DB 61 VINGSGFGVYVQAKLCSGSELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 120
 QY 131 EKKDEVYLVLDVPEPTVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 190
 DB 121 EKKDEVYLVLDVPEPTVYRVARHYSRAKQALPIYVKLYMYQLFRSLAYHSFGICHR 180
 QY 191 DIKPQNLLDPDTRVTLKLCDFGSAKQIVRGEPNVSYSRYRAPBELIFGATDTSIDV 250
 DB 181 DIKPQNLLDPDTRVTLKLCDFGSAKQIVRGEPNVSYSRYRAPBELIFGATDTSIDV 240
 QY 251 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTRQIREFMNPYTEFKEPQIKAMP 310
 DB 241 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTRQIREFMNPYTEFKEPQIKAMP 300
 QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
 QY 371 NFTQELSSNPPLATTIIPPHAR 393
 DB 361 NFTQELSSNPPLATTIIPPHAR 383

RESULT 10
 Q91627_XENLA PRELIMINARY; PRT; 420 AA.

ID Q91627;
 AC Q91627;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Glycogen synthase kinase 3 beta.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95396823; PubMed=7667318;
 RA Dominguez I., Itoh K., Sokol S.Y.,
 RT "Role of glycogen synthase kinase 3 beta as a negative regulator of
 RT dorsoventral axis formation in Xenopus embryos.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:8498-8502(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: U31862; AA84444.1; -; mRNA.
 DR PIR: I51692; I51692.
 DR HSSP: P49841; 1109.
 DR SMK: Q91627; 23-386.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR008271; Ser_Thr_kin_AS.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SMO0220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00106; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 420 AA; 46900 MW; 4FECCEA381835BFC7 CRC64;

Query Match 92.4%; Score 1923; DB 2; Length 420;
 Best Local Similarity 95.0%; Pred. No. 8,2e-125;
 Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVOQPSAFGSMKYSRDKGSKTTTVAATPGQDPDRQEVSYDTK 70
 DB 1 MSGRPRTTSFAESCKPVOQPSAFGSMKYSRDKGSKTTTVAATPGQDPDRQEVSYDTK 60
 QY 71 VINGSGFGVYVQAKLCSGSELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 130
 DB 61 VINGSGFGVYVQAKLCSGSELVAIKKVLQDKRFKRNRELOMRKLDHCNIVLRFFYSYG 120
 QY 131 EKKDEVYLVLDVPEPTVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 190
 DB 121 EKKDEVYLVLDVPEPTVYRVARHYSRAKQALPIYVKLYMYQLFRSLAYHSFGICHR 180
 QY 191 DIKPQNLLDPDTRVTLKLCDFGSAKQIVRGEPNVSYSRYRAPBELIFGATDTSIDV 250
 DB 181 DIKPQNLLDPDTRVTLKLCDFGSAKQIVRGEPNVSYSRYRAPBELIFGATDTSIDV 240
 QY 251 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTRQIREFMNPYTEFKEPQIKAMP 310
 DB 241 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTRQIREFMNPYTEFKEPQIKAMP 300
 QY 311 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
 QY 371 NFTQELSSNPPLATTIIPPHAR 393
 DB 361 NFTQELSSNPPLATTIIPPHAR 383

RESULT 11
 Q4SOHO_TETNG PRELIMINARY; PRT; 496 AA.

ID Q4SOHO;
 AC Q4SOHO;
 DT 13-SEP-2005 (TREMblrel. 31, Created)
 DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
 DE Chromosome 2 SCAF14781, whole genome shotgun sequence.
 GN ORFNames=GSTENG0026022001;
 OS Tetradodon nigroviridis (Green puffer).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Tetraodontidae; Tetraodon.
 NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Benoit A.,
 RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellil V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Castolico L., Poulin J., De Bernardis V.,
 RA Craud C., Duprat S., Brottier P., Couranceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellie M., Wolff J.N., Guigo R., Zody M.C., Meitov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope: Whitehead Institute Centre for Genome Research;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- FUNCTION: Plays a key role in the control of the eukaryotic cell

CC cycle. It is required in higher cells for entry into S-phase and
 CC mitosis. Component of the kinase complex that phosphorylates the
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of
 CC MPP (by similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 CC mature oocytes (by similarity).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: CA601014781; CAG05862.1; -1 Genomic DNA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 2.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; Tyr_k; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR KEGG: ATP-binding; Kinase; Nucleotide-binding;
 KM Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 496 AA; 55961 MW; 4C86362BD3301390 CRC64;

Query Match 86.2%; Score 1793.5; DB 2; Length 496;
 Best Local Similarity 73.8%; Pred. No. 9e-116;
 Matches 354; Conservative 8; Mismatches 3; Indels 115; Gaps 3;

QY 11 MSGRRPTTSFASCKPVOQPSAFSGSMKYSR-----DKDGSKYTTVAATPGCGPRP 61
 DB 1 MSGRRPTTSFASCKPVOQPSAFSGSMKYSRQTNGPWRGDDKDGSKYTTVAATPGCGPRP 60
 QY 62 QEVSTYDTKVIKNGSGFVYVYQAKLCDSEGLVAIKKVLQDKPKNELQIMKLDHCNIVR 121
 DB 61 QEVSTYDTKVIKNGSGFVYVYQAKLCDSEGLVAIKKVLQDKPKNELQIMKLDHCNIVR 120
 QY 122 LRFYFSSGSK----- 132
 DB 121 LRFYFSSGSKPDRRRANRPSVSNMVTGELSQLRCKPCSQLTRAVQAQSGQEP1R 180
 QY 133 -----KDEYVLANLVLY 145
 DB 181 PSGNPCKMLCRGRKSLFLRESANKVDFPQVPRSRGHSVRSKSDDEVYLANLVLY 240
 QY 146 PETVYVARVARYSRKQTLPIVYVKLYMQLYQFSLAYIHSFGICHRDIPKQMLLDPDPAV 205
 DB 241 PETVYVARVARYSRKQTLPIVYVKLYMQLYQFSLAYIHSFGICHRDIPKQMLLDPDPAV 300
 QY 206 LKLCDFGSAKQLVGEPNVSYICSTRYRAPBLIFGATDTYSSIDVWSAGCVLAELLQOP 265
 DB 301 LKLCDFGSAKQLVGEPNVSYICSTRYRAPBLIFGATDTYSSIDVWSAGCVLAELLQOP 360
 QY 266 IFPGDSGVDOLEVIK-----VLGTPFREQIREMNPVYEFKFPQIKAHPMYKVF 315
 DB 361 IFPGDSGVDOLEVIKQNAAPRSQVLTGTPFREQIREMNPVYEFKFPQIKAHPMYKVF 420
 QY 316 RPRTPPEAIALCSRLLEYTPARLTPLEACASFPDELDPNVKHPNGRDTPALFNFTTQ 375
 DB 421 RPRTPPEAIALCSRLLEYTPARLTPLEACASFPDELDPNVKHPNGRDTPALFNFTTQ 480

RESULT 12
 Q9YH61 BRARE
 ID Q9YH61 BRARE PRELIMINARY; PRT; 440 AA.
 AC Q9YH61
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Glycogen synthase kinase 3 alpha.
 OS Name=gsk3a; Synonym=gSK3;
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20171069; PubMed=10704871; DOI=10.1016/S0925-4773(99)00300-7;
 RA Tsai J.N., Lee C.H., Jeng H., Chi W.K., Chang W.C.;
 RT "Differential expression of glycogen synthase kinase 3 genes during
 RT zebrafish embryogenesis.";
 RL Mech. Dev. 91:387-391(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shamen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Binkley R.W., Touchman J.W., Green E.D., Dickson W.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RG NIH MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Straubeberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AJ223501; CA11419.1; -; mRNA.
 DR EMBL: BC065952; AAH65952.1; -; mRNA.
 DR EMBL: BC065332; AAH6332.1; -; mRNA.
 DR HSSP: P49841; 1Q3W.
 DR SMR: Q9YH61; 52-412.
 DR Ensembl: ENSDARG0000015681; Danio rerio.
 DR ZFIN: ZDB-GENE-990714-3; gsk3a.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 440 AA; 48065 MW; 66A8B8D070AC2093 CRC64;

Query Match 81.9%; Score 1704.5; DB 2; Length 440;
 Best Local Similarity 79.1%; Pred. No. 1.1e-109;
 Matches 326; Conservative 26; Mismatches 25; Indels 35; Gaps 3;

QY 12 SGRPRITTSFASCKPVOQPSAFSGSMKYSR-----SAFGSMKYSRD 41

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Db 4 SGRRTSSFAE---PGVPGAAAAAAGSAVAGSSSGKTGGAQAAGSSSSGFGNLKXGR- 59
Qy 42 KDGSKVTTVVATPGQGPDRPOEVSYTDTKYINGSGFGVYVQAALCDSGELVAIKVLQDK 101
Db 60 -DSGKVTTVVATPGQGPDRPOEVSYTDTKYINGSGFGVYVQAALCDSEMAIKKVLQDK 118
Qy 102 RFKRELOIMRKLDHCHNIVLRIRFFYSSEKKEDEVYLNVLVDYVPEYVVAHHYSPRAKQ 161
Db 119 RFKRELOIMRKLDHCHNIVLRIRFFYSSEKKEDEVYLNVLVDYVPEYVVAHHYSPRAKQ 178
Qy 162 TLPIYVKLYMYQLFRSLAYIHSGVCHRDIKPQNLILDPDPAVLKLCDFGSAKQVLRGE 221
Db 179 TIFPIYKVMYQLFRSLAYIHSGVCHRDIKPQNLILDPDPAVLKLCDFGSAKQVLRGE 238
Qy 222 PNVSYICSRYRRABELIFGATDYTSNIDWSAGCVLAELLGQPIFGDSGVQDLVEIIT 281
Db 239 PNVSYICSRYRRABELIFGATDYTSNIDWSAGCVLAELLGQPIFGDSGVQDLVEIIT 298
Qy 282 VLGPTRERQIRENNPNYTEKFPQIKAHPTKVFRRPTPEAIALCSRLLEYTPARLTP 341
Db 299 VLGPTRERQIRENNPNYTEKFPQIKAHPTKVFRRPTPEAIALCSRLLEYTPARLTP 358
Qy 342 LEACAHSFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 359 LEACAHSFDELRDPNVKHPNGRDTPALFNTTQELSSNPPLATILIPPHAR 410

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RESULT 13
Q9IBD3 BRARE
ID 09IBD3 BRARE PRELIMINARY; PRT; 435 AA.
AC 09IBD3
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Glycogen synthase kinase 3 alpha.
GN Name=gsk3a;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN NM_017105.1
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20171051; PubMed=10704853; DOI=10.1016/S0925-4773(99)00319-6;
RA Shimizu T., Yamamaki Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
RA Bae Y.-K., Hibi M., Hirano T.,
RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
RT formation of the dorsal organizer in zebrafish.";
RL Mech. Dev. 91:293-303(2000).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB032264; BAA92441.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMK; Q9IBD3; 52-412.
DR Ensembl; ENSDARG00000029723; Danio rerio.
DR ZFIN; ZDB-GENE-990714-3; gsk3a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 435 AA; 47791 MW; ED77993A03D8C706 CRC64;

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Query Match 80.2%; Score 1669.5; DB 2; Length 435;
Best Local Similarity 78.2%; Pred. No. 2,9e-107;
Matches 322; Conservative 26; Mismatches 29; Indels 35; Gaps 3;
Qy 12 SGRRTSSFAECPKVPQOP-----SAFGSKVSRD 41
Db 4 SGRRTSSFAE---PGVPGAAAAAAGSAVAGSSSGKTGGAQAAGSSSSGFGNLKXGR- 59
Qy 42 KDGSKVTTVVATPGQGPDRPOEVSYTDTKYINGSGFGVYVQAALCDSGELVAIKVLQDK 101
Db 60 -DSGKVTTVVATPGQGPDRPOEVSYTDTKYINGSGFGVYVQAALCDSEMAIKKVLQDK 118
Qy 102 RFKRELOIMRKLDHCHNIVLRIRFFYSSEKKEDEVYLNVLVDYVPEYVVAHHYSPRAKQ 161
Db 119 RFKRELOIMRKLDHCHNIVLRIRFFYSSEKKEDEVYLNVLVDYVPEYVVAHHYSPRAKQ 178
Qy 162 TLPIYVKLYMYQLFRSLAYIHSGVCHRDIKPQNLILDPDPAVLKLCDFGSAKQVLRGE 221
Db 179 TIFPIYKVMYQLFRSLAYIHSGVCHRDIKPQNLILDPDPAVLKLCDFGSAKQVLRGE 238
Qy 222 PNVSYICSRYRRABELIFGATDYTSNIDWSAGCVLAELLGQPIFGDSGVQDLVEIIT 281
Db 239 PNVSYICSRYRRABELIFGATDYTSNIDWSAGCVLAELLGQPIFGDSGVQDLVEIIT 298
Qy 282 VLGPTRERQIRENNPNYTEKFPQIKAHPTKVFRRPTPEAIALCSRLLEYTPARLTP 341
Db 299 VLGPTRERQIRENNPNYTEKFPQIKAHPTKVFRRPTPEAIALCSRLLEYTPARLTP 358
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RESULT 14
Q9NL43 CIOIN
ID 09NL43 CIOIN PRELIMINARY; PRT; 407 AA.
AC 09NL43
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Glycogen synthase kinase alpha/beta.
GN Name=CiGSK; Synonyms=Ci-GSK alpha/beta;
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cloniidae; Clona.
OC NCBI_TaxID=7719;
RN NM_017105.1
RP NUCLEOTIDE SEQUENCE.
RA Imai K., Takada N., Satoh Y.,
RT Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN NM_017105.1
RP NUCLEOTIDE SEQUENCE.
RA Satou Y., Satoh N.,
RT "Expressed genes in Clona intestinalis.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB031544; BAA92186.1; -; mRNA.
DR EMBL; AB211133; BAE06824.1; -; mRNA.
DR HSSP; P49841; 1Q3W.
DR SMK; Q9NL43; 9-368.
DR Ensembl; ENSCING00000001821; Clona intestinalis.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KM Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 407 AA; 45566 MW; E71594A9B6B59F10 CRC64;

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Query Match 80.1%; Score 1666.5; DB 2; Length 407;
 Best Local Similarity 83.0%; Pred. No. 4.4e-107;
 Matches 318; Conservative 24; Mismatches 26; Indels 15; Gaps 2;

QY 11 MSGRPTTSFAESCKRVQPSAFGSMKVSARDKSGKVTIVVATPGGPPRPOEVSYTDK 70
 DB 1 MEGAPKTI-----LGNMKGSRDKE-SKITTVATHGHGPRRQEVATTDK 45
 QY 71 VINGSGFGVYQAKLCDSEGLVAIKKVLQDKRPFKNRELQIMRDLHCNIVRLRFFYS 130
 DB 46 VINGSGFGVYQAKRIESENEMVAIKKVLQDKRPFKNRELQIMRDLHCNIVRLRFFYS 105
 QY 131 EKKDEYVNLVDYVETVYRVARHRSRAKQTLPIVYVLYMYQLFRSLAYIHSFGICHR 190
 DB 106 DKDEYVNLVDYVETVYRVARHRSRAKQTLPIVYVLYMYQLFRSLAYIHSFGICHR 165
 QY 191 DIKPNLLDPTAVLKCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYTSIDV 250
 DB 166 DIKPNLLDPTAVLKCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYTSIDV 225
 QY 251 WSAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKIAPH 310
 DB 226 WSAGCVLAEILLGQPIFPDSDGVDQVLEIKVLGTPTRQIREMNPNTYEFKPKIAPH 285
 QY 311 WTKVPRPTPPPEALACSLRLLEYTPARLTPLEACHSFDELDPNVKHPGRDTPALF 370
 DB 286 WSKVPRPTPPPEALACSLRLLEYTPARLTPLEACHSFDELDPNVKHPGRDTPALF 345
 QY 371 NFTTOELSSNPPLATILIPPHAR 393
 DB 346 NFTDKELGSKSPILNILLIPPHAR 368

RESULT 15
 Q6UG5 LYTV A PRELIMINARY; PRT; 414 AA.
 ID Q6UG5 LYTV A PRELIMINARY; PRT; 414 AA.
 AC Q6UG5-
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Glycogen synthase kinase-3.
 GN Name=GSK-3;
 OS Lytechinus variegatus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7654;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed15151983; DOI=10.1242/dev.01152;
 RA Weitzel H.E., Illies M.R., Byrum C.A., Xu R., Wikramanayake A.H.,
 RA Ettensohn C.A.;
 RT "Differential stability of {beta}-catenin along the animal-vegetal
 RT axis of the sea urchin embryo mediated by dishevelled";
 RL Development 131.2947-2956(2004).
 CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC EMBL; AY624076; AAT42372.1; -; mRNA.
 DR HSSP; P24941; IAO1.
 DR SMR; Q6UG5; 23-381.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 414 AA; 46202 MW; 276988692DF90815 CRC64;

Query Match 78.4%; Score 1632; DB 2; Length 414;
 Best Local Similarity 80.5%; Pred. No. 1.1e-104;
 Matches 306; Conservative 35; Mismatches 37; Indels 2; Gaps 1;

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 QY 72 IINGSGFGVYQAKLCDSEGLVAIKKVLQDKRPFKNRELQIMRDLHCNIVRLRFFYS 131
 DB 62 IINGSGFGVYQAKRVMDTNDLVAIKKVLQDKRPFKNRELQIMRDLHCNIVRLRFFYS 121
 QY 132 KKDEYVNLVDYVETVYRVARHRSRAKQTLPIVYVLYMYQLFRSLAYIHSFGICHRD 191
 DB 122 KKDEYVNLVDYVETVYRVARHRSRAKQTLPIVYVLYMYQLFRSLAYIHSFGICHRD 181
 QY 192 IKPNLLDPTAVLKCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYTSIDV 251
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 QY 312 TKVPRPTPPPEALACSLRLLEYTPARLTPLEACHSFDELDPNVKHPGRDTPALF 371
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 QY 372 FTTTOELSSNPPLATILIPPH 391
 DB 362 FTAGELASKSPILNILLIPPH 381

Search completed: May 16, 2006, 15:09:33
 Job time : 232 secs

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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:09:51 ; Search time 45 Seconds
(without alignments)

723.872 Million cell updates/sec

Title: US-10-689-461-2

Sequence: 1 MEVYPMEGGSGSGRPRTTSF.....OELSSNPPLATILPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*

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4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep:*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	2	US-09-916-109-2
2	2081	100.0	394	2	US-10-211-412B-2
3	2024	97.3	420	2	US-09-336-038-1
4	2024	97.3	420	2	US-09-916-109-1
5	2024	97.3	420	2	US-10-211-412B-1
6	2024	97.3	420	2	US-09-538-092-1163
7	2010	96.6	420	1	US-08-602-264A-14
8	1883.5	90.5	361	2	US-09-916-109-3
9	1883.5	90.5	361	2	US-10-211-412B-3
10	1609	77.3	447	2	US-09-916-109-5
11	1609	77.3	447	2	US-10-211-412B-5
12	1609	77.3	483	2	US-09-916-109-4
13	1609	77.3	483	2	US-10-211-412B-4
14	1609	77.3	483	2	US-09-538-092-1162
15	1588	76.3	351	2	US-09-916-109-7
16	1588	76.3	351	2	US-10-211-412B-7
17	1588	76.3	387	2	US-09-916-109-6
18	1588	76.3	387	2	US-10-211-412B-6
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20	1256	60.4	412	2	US-09-854-731-21
21	1242	59.7	410	2	US-09-347-801-10
22	1242	59.7	410	2	US-09-854-731-10
23	1240	59.6	402	2	US-09-347-801-16
24	1240	59.6	402	2	US-09-854-731-16
25	1232	59.2	405	2	US-09-347-801-20
26	1232	59.2	405	2	US-09-854-731-20
27	1232	59.2	407	2	US-09-347-801-23

28	1232	59.2	407	2	US-09-854-731-23	Sequence 23, Appl
29	1226	58.9	411	2	US-09-347-801-22	Sequence 22, Appl
30	1226	58.9	411	2	US-09-854-731-22	Sequence 22, Appl
31	1165.5	56.0	399	2	US-09-347-801-14	Sequence 14, Appl
32	1165.5	56.0	399	2	US-09-854-731-14	Sequence 14, Appl
33	1001.5	48.1	395	2	US-09-248-796A-18499	Sequence 18499, A
34	940	45.2	370	2	US-09-538-092-623	Sequence 623, App
35	674	32.4	411	2	US-09-248-796A-18500	Sequence 18500, A
36	521.5	25.1	146	2	US-09-270-767-43078	Sequence 43078, A
37	483.5	23.2	649	2	US-09-949-016-10147	Sequence 10147, A
38	483.5	23.0	334	2	US-09-949-016-10147	Sequence 10147, A
39	476.5	22.9	379	2	US-09-411-628-14	Sequence 14, Appl
40	476.5	22.9	379	2	US-10-174-794-14	Sequence 14, Appl
41	476.5	22.9	379	2	US-09-538-092-1021	Sequence 1021, Ap
42	472.5	22.7	379	2	US-08-622-277A-8	Sequence 8, Appl
43	472.5	22.7	379	2	US-09-025-560-25	Sequence 25, Appl
44	472.5	22.7	379	2	US-09-642-749-25	Sequence 25, Appl
45	472.5	22.7	631	2	US-09-417-197-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1									
US-09-916-109-2									
Sequence 2, Application US/09916109									
Patent No. 6465231									
GENERAL INFORMATION:									
APPLICANT: Harrison, Stephen D.									
APPLICANT: Hall, John A.									
APPLICANT: Calderon-Cacia, Maria									
APPLICANT: Zhong, Ziyang									
APPLICANT: Pang, Eric Y.									
APPLICANT: Colt, Doris G.									
APPLICANT: Nguyen, Steve H.									
APPLICANT: Medina-Selby, Angelica									
TITLE OF INVENTION: GSK3 POLYPEPTIDES									
FILE REFERENCE: PP-15876.002/200130.524									
CURRENT APPLICATION NUMBER: US/09/916.109									
CURRENT FILING DATE: 2001-07-25									
NUMBER OF SEQ ID NOS: 11									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 2									
LENGTH: 394									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-916-109-2									
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Best Local Similarity 100.0%; Score 2081; DB 2; Length 394;									
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MEVYPMEGGSGSGRPRTTSFASCKPVQQAFAFGSMKVRDQDSKVTTVATPGQGPDR	60						
DB	1	MEVYPMEGGSGSGRPRTTSFASCKPVQQAFAFGSMKVRDQDSKVTTVATPGQGPDR	60						
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QY	121	RLRFPPSSGKKQDEYVNLVDYPPVYVVAHHYSAAKQTLPIYIKLIMYQLFRSLA	180						
DB	121	RLRFPPSSGKKQDEYVNLVDYPPVYVVAHHYSAAKQTLPIYIKLIMYQLFRSLA	180						
QY	181	YIHSFGCHRDIKPQNLIDPDTAVLKLCDGSAKQIVRGSPNYSICRYRABELIFG	240						
DB	181	YIHSFGCHRDIKPQNLIDPDTAVLKLCDGSAKQIVRGSPNYSICRYRABELIFG	240						
QY	241	ATDYTSIDVWSACVLAELLGQPIFGDSGVQDLVEIIRKVLGTPTRBOIRENNPNYTE	300						
DB	241	ATDYTSIDVWSACVLAELLGQPIFGDSGVQDLVEIIRKVLGTPTRBOIRENNPNYTE	300						
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Db 301 FKPFQIKAHPTKVFRRPTPEPAIALCSRLLEYTPATLTPLBACAHSFPELBDPNVKH 360
Qy 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
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RESULT 2

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US-10-211-412B-2
; Sequence 2, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US/10/211.412B
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-2
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Best Local Similarity 100.0%; Pred. No. 2.8e-221;
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Db 61 PQEVSYDTKVIKNGSGFVVYQAKLCSGSELVAIKKVLQDKRFKNRELQIMRKLDHCNIY 120
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Db 241 ATDYTSIDVWSAGCVLAELLGOPIFPGDSGVQLVEIIVLGPTRREOIRRMNPYTE 300
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Qy 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
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RESULT 3
US-09-336-038-1
; Sequence 1, Application US/09336038
; Patent No. 6417185
; GENERAL INFORMATION:
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; APPLICANT: Goff, Dane
; APPLICANT: Harrison, Steven
; APPLICANT: Nuse, John
; APPLICANT: Ring, David B.
; APPLICANT: Zhou, Xiaohu A.
; TITLE OF INVENTION: Inhibitors of Glycogen Synthase Kinase 3
; FILE REFERENCE: 1443.003
; CURRENT APPLICATION NUMBER: US/09/336.038
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/089.978
; EARLIER FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-038-1
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Best Local Similarity 100.0%; Pred. No. 6.3e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 71 VIKNGSGFVVYQAKLCSGSELVAIKKVLQDKRFKNRELQIMRKLDHCNIYRLRYFFYS 120
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Db 131 EKKDEVYLNLDVYPETVYRVARHYSRAKOTLPVIYVKLYMYQLFRSLAYISFGICHR 180
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Db 181 DIKQNLIDPDTAVLKCDFGSAKQIVRGEPNVSYICSRYRABELIFGATDYTSIDV 240
Qy 251 WSAGCVLAELLGOPIFPGDSGVQLVEIIVLGPTRREOIRRMNPYTEFKPFQIKAH 310
Db 241 WSAGCVLAELLGOPIFPGDSGVQLVEIIVLGPTRREOIRRMNPYTEFKPFQIKAH 300
Qy 311 WTKVFRPTPEPAIALCSRLLEYTPATLTPLBACAHSFPELBDPNVKH 370
Db 301 WTKVFRPTPEPAIALCSRLLEYTPATLTPLBACAHSFPELBDPNVKH 360
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Db 361 NFFTQELSSNPPLATILIPPHARI 384
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RESULT 4

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US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916.109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-1

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Query Match	97.3%	Score 2024;	DB 2;	Length 420;
Best Local Similarity	100.0%	Pred. No. 6.3e-215;		
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Qy	191	DIKPQNLILDPTAVLKLCDPFGSAQOLVAGBPNVSITCSRRYRAPELIFGATDYTSIDV	250
Db	181	DIKPQNLILDPTAVLKLCDPFGSAQOLVAGBPNVSITCSRRYRAPELIFGATDYTSIDV	240
Qy	251	WSAGCVLAEILLGQPIFPDGSVDQVLEIIKVLGTFTRQIRBMBNBYTEFKFPQIKAH	310
Db	241	WSAGCVLAEILLGQPIFPDGSVDQVLEIIKVLGTFTRQIRBMBNBYTEFKFPQIKAH	300
Qy	311	WTKVFRPPTPPEAIALCSRLLEYTPPAKLTPLEACAHSPFDELRDENVVHGNGRDTPALF	370
Db	301	WTKVFRPPTPPEAIALCSRLLEYTPPAKLTPLEACAHSPFDELRDENVVHGNGRDTPALF	360
Qy	371	NFTTOELSSNPPLATILIPPHARI	394
Db	361	NFTTOELSSNPPLATILIPPHARI	384

RESULT 5
US-10-211-412B-1

Sequence 1, Application US/10211412B
 Patent No. 6716624
 GENERAL INFORMATION:
 APPLICANT: Harrison, Stephen D.
 APPLICANT: Hall, John A.
 APPLICANT: Calderon-Garcia, Maria
 APPLICANT: Zhang, Ziyang
 APPLICANT: Fang, Eric Y.
 APPLICANT: Choi, Doris G.
 APPLICANT: Nguyen, Steve H.
 APPLICANT: Medina-Selby, Angelica
 TITLE OF INVENTION: GSK3 POLYPEPTIDES
 FILE REFERENCE: 59516-162/PP-15876.002/200130.52
 CURRENT APPLICATION NUMBER: US/10/211,412B
 CURRENT FILING DATE: 2002-07-31
 PRIOR APPLICATION NUMBER: US09/916,109
 PRIOR FILING DATE: 2001-07-25
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSeq for Windows Version 4.0

```
Query Match      97.3%; Score 2024; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 6.3e-215;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Oy 11 MSGRRRTTSPFASBCKRPVQOPSAFGSMKYSRDKGSKTTTVATPGCGPDRPGEVSTTDTK 70
| | | | |
Dd 1 MSGRRRTTSFABSCAPVQGPSAFGSMKYSRDDSGSKTTTVATPGGPDRPGSVSTTDTK 60
| | | | |
Oy 71 VIGNGSFGVVYQAKLDSGELVAIKKVLODKKFKNRELOIMRKLDHCNITVRLEFFPYSSG 130
| | | | |

Db	61	VIGNSFGVVOYQAKCDSEGLVAIKKVIQDQRFKKRELQIRKQKDHCNIVRLRYFFSSG	120
Qy	131	EKDEEYVNLVLVDYVPEITYRVARHYSBAKOTLPVIYVKLYMYOLFESLAYIHSFGICHR	190
Db	121	EKDEEYVNLVLVDYVPEITYRVARHYSBAKOTLPVIYVKLYMYOLFESLAYIHSFGICHR	180
Qy	191	DIPEQNLILDPDTAVLKLCDPFSAAQVYRGEPNNYSICSRYYRAPELIFGATDVTSSIDV	250
Db	181	DIPEQNLILDPDTAVLKLCDPFSAAQVYRGEPNNYSICSRYYRAPELIFGATDVTSSIDV	240
Qy	251	WSAGCVLAETLLGQPIFPEDSGVDQVLEIIKVLGTPTREQIRKNNPYTEKFEQIRAH	310
Db	241	WSAGCVLAETLLGQPIFPEDSGVDQVLEIIKVLGTPTREQIRKNNPYTEKFEQIRAH	300
Qy	311	WTKVFRPRTPEPAIALCSRLLEYTPAALTPLEACAHSFDELDPNVKHPNGRDPALF	370
Db	301	WTKVFRPRTPEPAIALCSRLLEYTPAALTPLEACAHSFDELDPNVKHPNGRDPALF	360
Qy	371	NFTTOELSSNPPLATILIPPHARI	394
Db	361	NFTTOELSSNPPLATILIPPHARI	384

RESULT 6
US-09-538-092-1163
? Sequence 1163, Application US/09538092

```

# Patent No 6753314
# GENERAL INFORMATION:
# APPLICANT: Glot, Loic
# APPLICANT: Manfred, Traci A.
# TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
# FILE REFERENCE: 15966-542
# CURRENT APPLICATION NUMBER: US/09/538,092
# CURRENT FILING DATE: 2000-03-29
# PRIOR APPLICATION NUMBER: 60/127,352
# PRIOR FILING DATE: 1999-04-01
# PRIOR APPLICATION NUMBER: 60/178,965
# PRIOR FILING DATE: 2000-02-01
# NUMBER OF SEQ ID NOS: 1387
# SOFTWARE: CuraPatsSeqFormatter Version 0.9
# SEQ ID NO 1163
# LENGTH: 420
# TYPE: PRT
# ORGANISM: Homo sapiens
# FEATURE:
# NAME/KEY: misc_feature
# LOCATION: (0)..(0)
# OTHER INFORMATION: Polypeptide Accession Number P49841
# US-09-538-092-1163

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Query Match	97.3%	Score 2024;	DB 2;	Length 420;
Best Local Similarity	100.0%;	Pred. No. 6.3e-215;		
Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

Db 241 MSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQEI REMNPYTEKFPQIKAMP 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 7
US-08-602-264A-14
Sequence 14, Application US/08602264A
Patent No. 5837853
GENERAL INFORMATION:
APPLICANT: AKIHiko TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE
TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: human being
US-08-602-264A-14

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 2,2e-213;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQOPSAFGSMKVSRLDKDSKVTTVVATPGQGPDRQEVSYDTK 70
Db 1 MSGRPRTTSFAESCKPVQOPSAFGSMKVSRLDKDSKVTTVVATPGQGPDRQEVSYDTK 60
QY 71 VIGSGSGVYVQAKLCSGSELVAIKKVLDQKRPKNRELQIMRKLDHNCIVLARFPYSSG 130
Db 61 LIGSGSGVYVQAKLCSGSELVAIKKVLDQKRPKNRELQIMRKLDHNCIVLARFPYSSG 120
QY 131 EKDEVLNLTVDVPEVTVVVAHYSRAKQTLPIVYKLYMQLFRSLAYIHSFGICHR 190
Db 131 EKDEVLNLTVDVPEVTVVVAHYSRAKQTLPIVYKLYMQLFRSLAYIHSFGICHR 190

Db 121 EKDEVLNLTVDVPEVTVVVAHYSRAKQTLPIVYKLYMQLFRSLAYIHSFGICHR 180
QY 191 DIKRONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYSRSRYRABELIFGATDVTSSIDV 250
Db 181 DIKRONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYSRSRYRABELIFGATDVTSSIDV 240
QY 251 MSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQEI REMNPYTEKFPQIKAMP 310
Db 241 MSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQEI REMNPYTEKFPQIKAMP 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVKHPNGDTPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 8
US-09-916-109-3
Sequence 3, Application US/09916109
Patent No. 6465231
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876, 002/200130,524
CURRENT APPLICATION NUMBER: US/09/916,109
CURRENT FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.8e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1 MEYVPMEGGMSGRPRTTSFAESCKPVQOPSAFGSMKVSRLDKDSKVTTVVATPGQGPDR 60
Db 1 MEYVPMEGG-----GSKVTTVVATPGQGPDR 27
QY 61 POEVSYTDITVINGSGGVYQAKLCSGSELVAIKKVLDQKRPKNRELQIMRKLDHNCIV 120
Db 28 POEVSYTDITVINGSGGVYQAKLCSGSELVAIKKVLDQKRPKNRELQIMRKLDHNCIV 87
QY 121 RLRFFYSSEKDEVLNLTVDVPEVTVVVAHYSRAKQTLPIVYKLYMQLFRSLA 180
Db 88 RLRFFYSSEKDEVLNLTVDVPEVTVVVAHYSRAKQTLPIVYKLYMQLFRSLA 147
QY 181 YIHSFGICHRDIPKONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYSRSRYRABELIFG 240
Db 148 YIHSFGICHRDIPKONLLDPDPAVYKLCDFGSAKOLVRGEPNVSYSRSRYRABELIFG 207
QY 241 ATDVTSSIDVMSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQEI REMNPYTE 300
Db 208 ATDVTSSIDVMSAGCVLAELLGQPIFGDSGVDQVLEIIKVLGTPTRQEI REMNPYTE 267
QY 301 FKRPQIAHWPVTVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVK 360
Db 268 FKRPQIAHWPVTVFRPRTPEPAIALCSRLLEYTPPTARLTPLBACAHSPFDELBDPVK 327
QY 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 394
Db 361 PNGRDTPALFNFTTQELSSNPPLATILIPPHARI 384

Db 328 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 361

RESULT 9
US-10-211-412B-3
Sequence 3, Application US/10211412B

Patent No. 6716624
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916.109
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-412B-3

Query Match 90.5%; Score 1883.5; DB 2; Length 361;
Best Local Similarity 91.6%; Pred. No. 1.8e-199;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 MEYPMEGGMSGRRTTSPAESCKPVQPSAFSGMSKVSRLDGSKTTTVAATPGCGDR 60
Db 1 MEYPMEGGSG-----GSKTTTVAATPGCGDR 27
Qy 61 PQEVSYTDTKYIGNSFGVYVQAKLCDGSELVAIKVLODKRFKRELOIMRKLDHCNIV 120
Db 28 PQEVSYTDTKYIGNSFGVYVQAKLCDGSELVAIKVLODKRFKRELOIMRKLDHCNIV 87
Qy 121 RLRYFFSYSGEKDESVYINLVDPETVYRVARHYSRAKQTLPIYVKLYMYOLFSLA 180
Db 88 RLRYFFSYSGEKDESVYINLVDPETVYRVARHYSRAKQTLPIYVKLYMYOLFSLA 147
Qy 181 YIHSGICHRDIKPNLLDPTAVLKCDFGSAKQLVGEPNVSYSRYRAPELIFG 240
Db 148 YIHSGICHRDIKPNLLDPTAVLKCDFGSAKQLVGEPNVSYSRYRAPELIFG 207
Qy 241 ATDVTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIRENNPNYTE 300
Db 208 ATDVTSSIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIRENNPNYTE 267
Qy 301 FKFPQIKAHPTKVFRRPTPEAIALCSRLLLEYPTARLTPLLEACASHFDELDPNVX 360
Db 268 FKFPQIKAHPTKVFRRPTPEAIALCSRLLLEYPTARLTPLLEACASHFDELDPNVX 327
Qy 361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 361

RESULT 10
US-09-916-109-5
Sequence 5, Application US/09916109
Patent No. 6465231
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang

APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/09/916.109
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-5

Query Match 77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6.1e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGMSGRPRT-TSPAESCCKPVQPSAFSGMSKVSRLDGSKTTTVAATPGCGDRPQEVSY 66
Db 73 GGGSGGPGAGTSPPP-----GVKLGR--DSGKTTTVAATPGCGPERSQEVAY 119
Qy 67 TDTKYIGNSFGVYVQAALCDGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRYF 126
Db 120 TDKYIGNSFGVYVQAALCDGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRYF 179
Qy 127 YSSGKDEYVNLVLDVPEPTVYRVARHYSRAKQTLPIYVKLYMYOLFSLAYHSFG 186
Db 180 YSSGKDEYVNLVLDVPEPTVYRVARHYSRAKQTLPIYVKLYMYOLFSLAYHSFG 239
Qy 187 ICHRDIKQNLNLDPTAVLKCDFGSAKQLVGEPNVSYSRYRAPELIFGATDYS 246
Db 240 VCHRDIKQNLNLDPTAVLKCDFGSAKQLVGEPNVSYSRYRAPELIFGATDYS 299
Qy 247 SIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIRENNPNYTEKFPQI 306
Db 300 SIDVWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPREQIRENNPNYTEKFPQI 359
Qy 307 KAHPTKVFRRPTPEAIALCSRLLLEYPTARLTPLLEACASHFDELDPNVKHPNGDT 366
Db 360 KAHPTKVFRRPTPEAIALCSRLLLEYPTARLTPLLEACASHFDELDPNVKHPNGDT 419
Qy 367 PALFNFPTTQELSSNPPLATILIPPHAR 393
Db 420 PALFNFPTTQELSSNPPLATILIPPHAR 446

RESULT 11
US-10-211-412B-5
Sequence 5, Application US/10211412B
Patent No. 6716624
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/PP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/211.412B
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916.109
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
TYPE: PRT

```

; ORGANISM: Homo sapiens
US-10-211-412B-5

Query Match      77.3%; Score 1609; DB 2; Length 447;
Best Local Similarity 80.6%; Pred. No. 6,1e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCCKPVQPSAFGSMKVSBDKDGSKVTTVVAATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTTVVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYLYNLVDYVPEYTVRVARHYSRAKOTLPVLYVYLWMQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYLYNLVLEVPETVYRVARHFTKAKLTIPILYVKYMWQLFRSLAYIHSOG 239

Qy 187 ICHRDIPQNLLDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIPQNLLVDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRCTGLQLPNNRPL 419

Qy 367 PALFNFTTOELSSNPPLATLILPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAIILIPHLR 446

RESULT 12
US-09-916-109-4
; Sequence 4, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 6,9e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCCKPVQPSAFGSMKVSBDKDGSKVTTVVAATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTTVVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYLYNLVDYVPEYTVRVARHYSRAKOTLPVLYVYLWMQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYLYNLVLEVPETVYRVARHFTKAKLTIPILYVKYMWQLFRSLAYIHSOG 239

Qy 187 ICHRDIPQNLLDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIPQNLLVDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 419
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Qy 127 YSSGEKDEYLYNLVDYVPEYTVRVARHYSRAKOTLPVLYVYLWMQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYLYNLVLEVPETVYRVARHFTKAKLTIPILYVKYMWQLFRSLAYIHSOG 239

Qy 187 ICHRDIPQNLLDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIPQNLLVDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 366
Db 420 PPLFNFSAGELSIQPSLNAIILIPHLR 446

RESULT 13
US-10-211-412B-4
; Sequence 4, Application US/10211412B
; Patent No. 6716624
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/211,412B
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412B-4

Query Match      77.3%; Score 1609; DB 2; Length 483;
Best Local Similarity 80.6%; Pred. No. 6,9e-169;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

Qy 8 GGGGSGRPRT-TSPAESCCKPVQPSAFGSMKVSBDKDGSKVTTVVAATPGGPRPDEVS 66
Db 73 GGGGSGGPGAGTSPFP-----GVLGR--DSGKVTTVVATLGGGPRSGEVAY 119

Qy 67 TDTKVIENGSGFVVYQAKLCDSGELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 126
Db 120 TDIKVIENGSGFVVYQARLAETRELVAIKVYLQDKRFKRNRELQIMRKLDCNIVRLRYFF 179

Qy 127 YSSGEKDEYLYNLVDYVPEYTVRVARHYSRAKOTLPVLYVYLWMQLFRSLAYIHSFG 186
Db 180 YSSGEKDEYLYNLVLEVPETVYRVARHFTKAKLTIPILYVKYMWQLFRSLAYIHSOG 239

Qy 187 ICHRDIPQNLLDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRDIPQNLLVDPDPAVLKLCDFGSAKQLVGEPNVSYICSRYYRAPELIFGATDYS 299

Qy 247 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 306
Db 300 SIDWMSAGCVLAELLLGQPIFPDGSVDQVLEIIVKLGTPREQIREMNPNTYEFKFPQI 359

Qy 307 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 366
Db 360 KAHFWTVFRRPTPEPAIALCSRLLEYTPPARLTPLCAHSPFDELRDPNVKHPNGRDT 419
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Db      360 KAHPTKPKFKSTPPEALALCSSLEETPSSRLSPLEACAHSPFDELRCGLQLPNNRPL 419
Qy      367 PALFNFTTOELSSNPPLATILIPPHAR 393
Db      420 PPLFNFSAGELSLQPSLNAIILIPHLR 446
```

RESULT 14

```
US-09-538-092-1162
; Sequence 1162, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Manifest, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1162
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P49840
US-09-538-092-1162
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Query Match 77.3%; Score 1609; DB 2; Length 483;

Best Local Similarity 80.6%; Pred. No. 6,9e-169; Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3;

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Qy      8 GCGSGMRPRT-TSFAESCKPVQPSAFSGSMKVSRLDKSGKVTTVVATPGQFDRPOEVSX 66
Db      73 GCGSGGGRGAGTSFPP-----GVKLGR--DSGKVTTVVATLGGQSPERGQVAY 119
Qy      67 TDTKVIKNGSGGVVYQAKLCSGELVAIKVLODYRFKRRRLQIRKLDHCNIVRLRYFF 126
Db      120 TDIKVIKNGSGFGVVYQARLAETRELVAIKVLODYRFKRRRLQIRKLDHCNIVRLRYFF 179
Qy      127 YSSGSKDEVTNLVDVPEETVYVAVRHYSRAKOTLPVYKLYMYQLFRSLAYIHSRG 186
Db      180 YSSGSKDEVTNLVDVPEETVYVAVRHYSRAKOTLPVYKLYMYQLFRSLAYIHSRG 239
Qy      187 ICHRDIKPQNLILDDPTAVLKLCDFGSAKQLVGSPNYSICSRYYRAPELIFGATDYTS 246
Db      240 VCHRIKQNLILVDDPTAVLKLCDFGSAKQLVGSPNYSICSRYYRAPELIFGATDYTS 299
Qy      247 SIDVMSACVLAELLGQPIFPDGSQVDQVEIIVLGTPTREQIREMNPNTSEKFPQI 306
Db      300 SIDVMSACVLAELLGQPIFPDGSQVDQVEIIVLGTPTREQIREMNPNTSEKFPQI 359
Qy      307 KAHPTKVPKSTPPEALALCSSLEETPSSRLSPLEACAHSPFDELRCGLQLPNNRPL 419
Db      360 KAHPTKVPKSTPPEALALCSSLEETPSSRLSPLEACAHSPFDELRCGLQLPNNRPL 419
Qy      367 PALFNFTTOELSSNPPLATILIPPHAR 393
Db      420 PPLFNFSAGELSLQPSLNAIILIPHLR 446
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RESULT 15
US-09-916-109-7
; Sequence 7, Application US/09916109
; Patent No. 6465231
; GENERAL INFORMATION:
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; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacila, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Cole, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-7
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Query Match 76.3%; Score 1588; DB 2; Length 351;

Best Local Similarity 86.2%; Pred. No. 8,6e-167; Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

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Qy      46 KVTTVVATPGQFDRPOEVSYTDPTKVIKNGSGFGVVYQAKLCSGELVAIKVLODYRFKRN 105
Db      3 KVTTVVATLGGQSPERGQVAYTDIKVIGNSFGVVYQARLAETRELVAIKVLODYRFKRN 62
Qy      106 RELQIMRLDHCNIVRLRYFFYSSGSKDEVTNLVDVPEETVYVAVRHYSRAKOTLPV 165
Db      63 RELQIMRLDHCNIVRLRYFFYSSGSKDEVTNLVDVPEETVYVAVRHYSRAKOTLPV 122
Qy      166 IYVKLYMYQLFRSLAYIHSFGICHRDIPQNLILDDPTAVLKLCDFGSAKQLVGSPNVS 225
Db      123 LVYKLYMYQLFRSLAYIHSFGICHRDIPQNLILDDPTAVLKLCDFGSAKQLVGSPNVS 182
Qy      226 YICSRYYRAPELIFGATDYTSIDVMSACVLAELLGQPIFPDGSQVDQVEIIVLGT 285
Db      183 YICSRYYRAPELIFGATDYTSIDVMSACVLAELLGQPIFPDGSQVDQVEIIVLGT 242
Qy      286 PIREQIREMNPNTSEKFPQIKAHPTKVPKSTPPEALALCSSLEETPSSRLSPLEAC 345
Db      243 PIREQIREMNPNTSEKFPQIKAHPTKVPKSTPPEALALCSSLEETPSSRLSPLEAC 302
Qy      346 AHSFPDELRCGLQLPNNRPLPPLFNFSAGELSLQPSLNAIILIPHLR 393
Db      303 AHSFPDELRCGLQLPNNRPLPPLFNFSAGELSLQPSLNAIILIPHLR 350
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Search completed: May 16, 2006, 15:11:10
Job time : 46 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:05:56 ; Search time 41 Seconds
(without alignments)
924.620 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081

Sequence: 1 MEYPMEGGSGMSGRPTTSF.....QELSNPLPALTLLPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	97.3	420	1	glycogen synthase
2	2010	96.6	420	1	tau-protein kinase
3	1931	92.8	420	2	intracellular kinase
4	1923	92.4	420	2	glycogen synthase
5	1607	77.2	483	1	protein kinase (EC
6	1590.5	76.4	575	2	protein kinase sgg
7	1542.5	74.1	733	2	probable protein k
8	1542.5	74.1	1067	2	protein kinase sgg
9	1342.5	64.5	362	2	hypothetical prote
10	1296	62.3	409	2	shaggy protein kin
11	1275.5	61.3	471	2	shaggy protein kin
12	1273.5	61.2	471	1	shaggy protein kin
13	1265	60.8	408	1	protein kinase MSK
14	1258	60.5	472	1	serine/threonine-s
15	1256	60.4	412	1	protein kinase MSK
16	1249	60.0	403	2	probable shaggy-li
17	1249	60.0	431	2	shaggy protein kin
18	1247.5	59.9	469	1	shaggy protein kin
19	1246	59.9	409	1	protein kinase ASK
20	1245	59.8	412	2	shaggy-like protei
21	1244	59.8	411	1	tau-protein kinase
22	1239	59.5	409	1	shaggy-like protei
23	1234	59.3	380	2	shaggy-like protei
24	1233	59.3	412	2	probable shaggy-li
25	1232	59.2	407	2	shaggy-like protei
26	1232	59.1	420	2	probable glycogen
27	1229.5	59.1	469	1	shaggy protein kin
28	1229.5	59.1	469	1	hypothetical prote
29	1228.5	59.0	447	2	

30	1226	58.9	411	1	protein kinase MSK
31	1226	58.9	468	2	shaggy-like protei
32	1220	58.6	421	2	protein kinase Akt
33	1208	58.0	447	2	hypothetical prote
34	1178	56.6	468	2	protein kinase (EC
35	1158	55.6	431	2	shaggy-like kinase
36	1156.5	55.6	387	2	protein kinase akt
37	1109.5	53.3	354	2	protein kinase akt
38	996	47.9	381	2	serine-threonine p
39	996	47.9	390	2	glycogen synthase
40	978.5	47.0	452	2	glycogen synthase
41	940.5	45.2	354	2	hypothetical prote
42	940	45.2	370	2	protein kinase RIM
43	873.5	42.0	501	2	WRI protein - yea
44	792	38.1	211	2	probable serine/th
45	735.5	35.3	367	2	hypothetical prote

ALIGNMENTS

RESULT 1
S53324
Glycogen synthase kinase 3 beta (EC 2.7.1.-) - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S53324
R:Stambolic, V.; Woodgett, J.R.
Biochem. J. 303, 701-704, 1994
A:Title: Mitogen inactivation of glycogen synthase kinase-3-beta in intact cells via ser
A:Reference number: S53324; PMID:95071278; PMID:7980435
A:Accession: S53324
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-420 <STA>
A:Cross-references: UNIPROT:P49841; UNIPARC:UPI00004839D; EMBL:L33801; NID:G529236; PID
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Comment: This enzyme is inhibited by phosphorylation of serine 9 by p70 S6 kinase (see
C:Genetics:
A:Gene: GSK3B
A:Cross-references: GDB:6108057
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:9/Binding site: phosphate (Ser) (covalent) (by ribosomal protein S6 kinase) #status ex
F:85/Active site: Lys #status predicted
Query Match 97.3%; Score 2024; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-89;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRTTSFASCKPVOQPSAFSGMKVSRKDSKYTTVAATPDGQDPDPOEVSYTQK 70
Db 1 MSGRPRTTSFASCKPVOQPSAFSGMKVSRKDSKYTTVAATPDGQDPDPOEVSYTQK 60
QY 71 VINGSGFQGVVYQALKCDGSELVAIKVYQDRFPKRLQIRKLDHCNIVLRFFYSSG 130
Db 61 VINGSGFQGVVYQALKCDGSELVAIKVYQDRFPKRLQIRKLDHCNIVLRFFYSSG 120
QY 131 EKQDEVTINLVLDVPEPTVVARHYSRAKQTLVYIYKLYMYQLFRSLAYIHSGICHR 190
Db 61 EKQDEVTINLVLDVPEPTVVARHYSRAKQTLVYIYKLYMYQLFRSLAYIHSGICHR 180
QY 121 EKQDEVTINLVLDVPEPTVVARHYSRAKQTLVYIYKLYMYQLFRSLAYIHSGICHR 180
Db 121 EKQDEVTINLVLDVPEPTVVARHYSRAKQTLVYIYKLYMYQLFRSLAYIHSGICHR 180
QY 191 DIKQNLILDDPTVAIVLKICDGSAGKOLVRGEPNYSICSRYYRAPELLFGATDYSIDV 250
Db 181 DIKQNLILDDPTVAIVLKICDGSAGKOLVRGEPNYSICSRYYRAPELLFGATDYSIDV 240
QY 251 WSACCVLAELLGQPIFFGDSGVQDLVEIIVKLGTPTRBOQIRENNPNYTEKFPQIKAP 310
Db 241 WSACCVLAELLGQPIFFGDSGVQDLVEIIVKLGTPTRBOQIRENNPNYTEKFPQIKAP 300
QY 311 WTKVFRPRTTPPALALCALCRLLLETTPTARLTPLKCAHSFFDELADPNVAKHNGRDTPLAF 370

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Db 301 WTKFRRTPEPALALCSRLLEYTPTRALTPLERCAHSFDELDPNVKHNQDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 2
TVRTKB
tau-protein kinase (EC 2.7.1.135) I - rat
N:Alternate names: factor A; glycogen synthase kinase 3 beta; protein kinase GSK-3-beta;
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S14708; S33741; S36723
R:Woodgett, J.R.
EMBO J. 9, 2431-2438, 1990
A:Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
A:Reference number: S14707; MUID:90316097; PMID:2164470
A:Accession: S14708
A:Molecule type: mRNA
A:Residues: 1-420 <WOO>
A:Cross-references: UNIPROT:P18266; UNIPARC:UPI000012DDC0; EMBL:X53428; NID:956333; PIDN
A:Note: the author translated the codon ATG for residue 240 as Val
R:Ichiguro, K.; Shiratsuchi, A.; Sato, S.; Omori, A.; Arioka, M.; Kobayashi, S.; Uchida,
FEBS Lett. 325, 167-172, 1993
A:Title: Glycogen synthase kinase 3-beta is identical to tau protein kinase I generating
A:Reference number: S33741; MUID:93307488; PMID:7686508
A:Accession: S33741
A:Molecule type: mRNA
A:Residues: 1-239, 'V', 241-420 <ISH>
A:Cross-references: UNIPARC:UPI00000018B4; EMBL:X73653; NID:g402651; PIDN:CAA52020.1; PI
A:Accession: S36729
A:Molecule type: protein
A:Residues: 37-58; 61-74; 151-158; 293-316; 318-325; 327-332; 351-368; 370-375 <ISH2>
A:Cross-references: UNIPARC:UPI0000172536; UNIPARC:UPI0000172537; UNIPARC:UPI0000172538;
S3D
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:85/Active site: Lys #status predicted

Query Match 96.6%; Score 2010; DB 1; Length 420;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;
Matches 382; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 3
151425
intracellular kinase (EC 2.7.1.-) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51425
R:Pierce, S.B.; Kimmel, D.
Development 121, 755-765, 1995
A:Title: Regulation of Spemann organizer formation by the intracellular kinase Xgsk-3.
A:Reference number: I51425; MUID:95237008; PMID:7720580
A:Accession: I51425
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-420 <PIE>
A:Cross-references: UNIPROT:Q91757; UNIPARC:UPI00000F8682; GB:L38492; NID:g727189; PIDN:
C:Genetics:
A:Gene: Xgsk-3
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:54-315/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif
F:85/Active site: Lys #status predicted

Query Match 92.8%; Score 1931; DB 2; Length 420;
Best Local Similarity 95.3%; Pred. No. 6.5e-85;
Matches 365; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
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Qy 11 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
Qy 71 VINGSGFGVYQAKLCTDSELVAIKVLDKRFKRNRELIQMRKLDHCNIYRLRFFYSYG 130
Db 61 VINGSGFGVYQAKLCTDSELVAIKVLDKRFKRNRELIQMRKLDHCNIYRLRFFYSYG 120
Qy 131 EKDEYVNLNVLVDVPEPTVVRVARRHYSRAQALPIIVKLYMQLFSLAYIHSGFCH 190
Db 121 EKDEYVNLNVLVDVPEPTVVRVARRHYSRAQALPIIVKLYMQLFSLAYIHSGFCH 180
Qy 191 DIRQNLLDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDTSIDV 250
Db 181 DIRQNLLDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDTSIDV 240
Qy 251 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPYTEFKFPQIKAH 310
Db 241 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPYTEFKFPQIKAH 300
Qy 311 WTKFRRTPEPALALCSRLLEYTPTRALTPLERCAHSFDELDPNVKHNQDTPALF 370
Db 301 WTKFRRTPEPALALCSRLLEYTPTRALTPLERCAHSFDELDPNVKHNQDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384
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Qy 11 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDTK 60
Qy 71 VINGSGFGVYQAKLCTDSELVAIKVLDKRFKRNRELIQMRKLDHCNIYRLRFFYSYG 130
Db 61 VINGSGFGVYQAKLCTDSELVAIKVLDKRFKRNRELIQMRKLDHCNIYRLRFFYSYG 120
Qy 131 EKDEYVNLNVLVDVPEPTVVRVARRHYSRAQALPIIVKLYMQLFSLAYIHSGFCH 190
Db 121 EKDEYVNLNVLVDVPEPTVVRVARRHYSRAQALPIIVKLYMQLFSLAYIHSGFCH 180
Qy 191 DIRQNLLDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDTSIDV 250
Db 181 DIRQNLLDPDTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDTSIDV 240
Qy 251 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPYTEFKFPQIKAH 310
Db 241 WSACCVLAELLGQPIFGDSGVQDLVEIIVLGTPTREQIREMNPYTEFKFPQIKAH 300
Qy 311 WTKFRRTPEPALALCSRLLEYTPTRALTPLERCAHSFDELDPNVKHNQDTPALF 370
Db 301 WTKFRRTPEPALALCSRLLEYTPTRALTPLERCAHSFDELDPNVKHNQDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384
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A:Cross-references: UNIPROT:Q91627; UNIPARC:UPI000006B937; EMBL:U11862; NID:g1000734; PDB:1A82
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP, phosphotransferase
 F:54-315/Domain: protein kinase homology <KIN>
 F:62-70/Region: protein kinase ATP-binding motif
 F:85/Active site: Lys #status predicted

Query Match 92.4%; Score 1923; DB 2; Length 420;
 Best Local Similarity 95.0%; Pred. No. 1.6e-84;
 Matches 364; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 11 MSGRRITTSFAESCPCVQOPSAFGSMKYSRDQSGSKTTTVAATPGQSPDRPOEVSYTDTK 70
 DB 1 MSGRRITTSFAESCPCVQOPSAFGSMKYSRDQSGSKTTTVAATPGQSPDRPOEVSYTDTK 60
 QY 71 VINGSGFVVYQAKLCDGELVAIKKVLQDKRFKNRELQIMKLDHCNIVRLRYFFYSG 130
 DB 61 VINGSGFVVYQAKLCDGELVAIKKVPQDKRFKNRELQIMKLDHCNIVRLRYFFYSG 120
 QY 131 EKQDEVYLNVLVDYPTETVYRVAHYRAKQTLPIYVKLYMYQLFRSLAYTHSGICHR 190
 DB 121 EKQDEVYLNVLVDYPTETVYRVAHYRAKQALPIIYVKLYMYQLFRSLAYTHSGICHR 180
 QY 191 DIKPNLLLDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRADELIFGATDYTSIDV 250
 DB 181 DIKPNLLLDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRADELIFGATDYTSIDV 240
 QY 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRERQIREMNPNTTEFKPQIKAMP 310
 DB 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRERQIREMNPNTTEFKPQIKAMP 300
 QY 311 WTKVRRPTPPPAIMLCGRLEYPTRARLTPEACAHSPFDELDRPNVAKHPGRTPPALF 370
 DB 301 WTKVRRPTPPPAIMLCGRLEYPTRARLTPEACAHSPFDELDRPNVAKHPGRTPPALF 360
 QY 371 NPTTQELSSNPPLATILIPPHAR 393
 DB 361 NPTTQELSSNPPLATILIPPHAR 383

RESULT 5
 TVRTKA

protein kinase (EC 2.7.1.37) GSK-3-alpha - rat
 N:Alternate names: factor A; glycogen synthase kinase 3 alpha
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: S14707
 R:Woodgett, J.R.
 EMBL J. 9, 2431-2438, 1990
 A:Title: Molecular cloning and expression of glycogen synthase kinase-3/Factor A.
 A:Reference number: S14707; MUID:90316097; PMID:2164470
 A:Accession: S14707
 A:Molecule type: mRNA
 A:Residues: 1-483 <RUB>
 A:Cross-references: UNIPROT:P18265; UNIPARC:UPI000012DBDF; EMBL:X53427; NID:g56331; PIDN:CA50215.1; PID:CA50215.1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP, phosphoprotein, phosphotransferase; serine/threonine-specific protein K
 F:117-378/Domain: protein kinase homology <KIN>
 F:125-133/Region: protein kinase ATP-binding motif
 F:148/Active site: Lys #status predicted

Query Match 77.2%; Score 1607; DB 1; Length 483;
 Best Local Similarity 80.6%; Pred. No. 1.6e-69;
 Matches 312; Conservative 23; Mismatches 38; Indels 14; Gaps 3;

QY 8 GGGMGRRRT--TSFASCKPVGQPPAFSGMKYSRDQSGSKTTTVAATPGQSPDRPOEVSX 66
 DB 73 GGGGGGSGAGTSFPP-----GVKLGK--DSGKVTTVVATGGGGERQGEVAY 119
 QY 67 TDTKIVNGSGFVVYQAKLCDGELVAIKKVLQDKRFKNRELQIMKLDHCNIVRLRYFF 126
 DB 120 TDIKIVNGSGFVVYQAKLAEIRLVAIKKVLQDKRFKNRELQIMKLDHCNIVRLRYFF 179

QY 127 YSSGKKDEVYLNVLVDYPTETVYRVAHYRAKQTLPIYVKLYMYQLFRSLAYTHSG 186
 DB 180 YSSGKKDEVYLNVLVDYPTETVYRVAHYRAKQTLPIYVKLYMYQLFRSLAYTHSG 239
 QY 187 ICHRDIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRADELIFGATDYTS 246
 DB 240 VCHRDIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRADELIFGATDYTS 299
 QY 247 SIDWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRERQIREMNPNTTEFKPQI 306
 DB 300 SIDWSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRERQIREMNPNTTEFKPQI 359
 QY 307 KAHPTKVRPTPPPAIMLCGRLEYPTRARLTPEACAHSPFDELDRPNVAKHPGRDT 366
 DB 360 KAHPTKVRPTPPPAIMLCGRLEYPTRARLTPEACAHSPFDELDRPNVAKHPGRDT 419
 QY 367 PALFNFTTQELSSNPPLATILIPPHAR 393
 DB 420 PPLFNFTTQELSSNPPLATILIPPHAR 446

RESULT 6
 S35327

protein kinase egg39 (EC 2.7.1.-) (clone pNB39) - fruit fly (Drosophila melanogaster)
 N:Alternate names: zw3-A
 N:Contains: protein kinase (EC 2.7.1.37)
 C:Species: Drosophila melanogaster
 C:Date: 19-Jul-1996 #sequence_revision 01-Nov-1996 #text_change 05-Oct-2004
 C:Accession: S35327; S35326; S35329; A44331; S11675; S10931; S35421; S35422; S35424
 R:Juel, L.; Partridge, V.; Lutz, Y.; Simpson, P.; Boutrouls, M.
 EMBL J. 12, 1657-1669, 1993

A:Title: Functional significance of a family of protein kinases encoded at the shaggy 10
 A:Reference number: S35325; MUID:93223707; PMID:8467811

A:Accession: S35327
 A:Molecule type: mRNA

A:Residues: 1-575 <RUB>
 A:Cross-references: UNIPROT:P18431; UNIPARC:UPI00002B384; EMBL:X70863; NID:g11145; PIDN:CA50215.1; PID:CA50215.1

A:Accession: S35326
 A:Molecule type: mRNA

A:Residues: 1-196, 'R', 198-394, 'D', 396-512, 'D', 514 <RUB>
 A:Cross-references: UNIPARC:UPI000016BD6A; EMBL:X70862; NID:g11143; PIDN:CA50212.1; PID:CA50212.1

A:Accession: S35329
 A:Molecule type: mRNA

A:Residues: 1-42 <RUB>
 A:Cross-references: UNIPARC:UPI000016BD6B; EMBL:X70865; NID:g11149; PIDN:CA50215.1; PID:CA50215.1

A:Accession: S35329
 A:Molecule type: mRNA

A:Residues: 1-445, 'R', 447-510, 'D', 512, 'D', 514 <RUB>
 A:Cross-references: UNIPARC:UPI000017A460; EMBL:X53332; NID:g10895; PIDN:CA50215.1; PID:CA50215.1

A:Accession: A44331
 A:Molecule type: mRNA

A:Residues: 1-445, 'R', 447-510, 'D', 512, 'D', 514 <RUB>
 A:Cross-references: UNIPARC:UPI000017A460; EMBL:X53332; NID:g10895; PIDN:CA50215.1; PID:CA50215.1

A:Accession: S11675
 A:Molecule type: mRNA

A:Residues: 1-243, 'I', 245-405, 'A', 407-512, 'D', 514 <BOU>
 A:Cross-references: UNIPARC:UPI000016BD69; EMBL:X53332; NID:g10895; PIDN:CA50215.1; PID:CA50215.1

A:Accession: S10931
 A:Molecule type: mRNA

A:Residues: 1-289 <S12>
 A:Cross-references: UNIPARC:UPI000016BE19; EMBL:X54005; NID:g8889; PIDN:CA50215.1; PID:CA50215.1

A:Experimental source: ovarian cDNA library

Qy 362 NGRDPALENFNTTQELSSNPPLATILIPPH 391
 |||||
 Db 904 NGRDMPPLFNTFHEHLSIQPSLVPLQLPRH 933

RESULT 9

T26520

hypothetical protein Y18D10A.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26520

R:Haris, B.
 submitted to the EMBL Data Library, December 1998

A:Accession: T26520

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-362 <MW>

A:Cross-references: UNIPROT:O9UZQ9; UNIPARC:UPI000007BD45; EMBL:AL034393; P1DN:CAA22311.

A:Experimental source: clone Y18D10A

C:GeneticB:

A:Gene: CESP:Y18D10A.5

A:Introns: 31/3; 121/2; 313/3

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 64.5%; Score 1342.5; DB 2; Length 362;

Best Local Similarity 77.2%; Pred. No. 4e-57;

Matches 254; Conservative 33; Mismatches 41; Indels 1; Gaps 1;

Qy 42 KDGSKVTIVVATPG-QGPDPRQEVSYTDTKVIKNGSGFVVYQAKLDSGELVAIKKVLQD 100
 |||||Db 11 KSGQVTVVAVASVATDGVDDQVEISYDQKVIKNGSGFVVYQAKLDSGELVAIKKVLQD 70
 |||||Qy 101 KRFKRRELQIRKLDHNCIVRLRYFYSSGKKDEVTNLVDVYBETVYRVARHYSRAK 160
 |||||Db 71 KRFKRRELQIRKLDHNCIVRLRYFYSSGKKDEVTNLVDVYBETVYRVARHYSRAK 130
 |||||Qy 161 QTLPLVYVYKLYMYQVFRGLAYTHSRGICHRDIPKQNLDPDTATLKI CDPSGAQVLRG 220
 |||||Db 131 QQIPITVYKLYMYQVFRGLAYTHSRGICHRDIPKQNLDPDTATLKI CDPSGAQVLRN 190
 |||||Qy 221 EPNVSYICRRYRABELIFGATDYSSIDVWSAGCVLAELLLGQIPFGDSGVQDLVEII 280
 |||||Db 191 EPNVSYICRRYRABELIFGATDYSSIDVWSAGCVLAELLLGQIPFGDSGVQDLVEII 250
 |||||Qy 281 KVLGTPTRQIRKEMNPNTTEFKPQIKAHPMWKVFRPTPEALACSRLLLEYTPARLT 340
 |||||Db 251 KVLGTPTRQIRKEMNPNTTEFKPQIKAHPMWKVFRPTPEALACSRLLLEYTPARLT 310
 |||||Qy 341 PLEKASHFDELDPNVKHPNGRDTPL 369
 |||||Db 311 PQAACOHAFDELNRNPDARLPGRPLPTL 339
 |||||

RESULT 10

S51105

shaggy protein kinase 4 (EC 2.7.1.1) - garden petunia

N:Alternate names: shaggy/zeeste-white 3 protein kinase homolog

C:Species: Petunia x hybrida (garden petunia)

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S51105

R:Decroocq-Ferrant, V.; van Went, J.; Bianchi, M.W.; de Vries, S.; Kreis, M.
 submitted to the EMBL Data Library, December 1994

A:Description: Petunia hybrida homologues of shaggy/zeeste-white 3 expressed in female ant

A:Reference number: S51105

A:Accession: S51105

A:Molecule type: mRNA

A:Residues: 1-409 <DEC>

A:Cross-references: UNIPROT:O40886; UNIPARC:UPI00000AA695; EMBL:X83619; NID:g619893; P1D

C:GeneticB:

A:Gene: PSK4

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphoprotein; phosphotransferase; protein kinase

F:72-332/Domain: protein kinase homology <KIN>
 F:80-88/Region: protein kinase ATP-binding motif
 F:103/Active site: Lys #status predicted

Query Match 62.3%; Score 1296; DB 2; Length 409;
 Best Local Similarity 62.3%; Pred. No. 7.1e-55;
 Matches 254; Conservative 49; Mismatches 75; Indels 30; Gaps 7;

Qy 4 MPMEGSGNSGRPTTSFASCKPVQGPASFMVSRK-----DSK----- 46

Db 6 MPASG----GKRTDAMLVD----KLPEINEMKIRDKAEKEMAAVVDNGTEKGHI 57

Qy 47 VTTVATPGQDPDRQEVSYTDTKVIKNGSGFVVYQAKLDSGELVAIKKVLQDGRFKNR 106
 |||||Db 58 VTTI---GGKNGBRKQITSYAERVVGSGSGIYQAKLETGERVAIKKVLQDGRYKNR 114
 |||||Qy 107 ELQIMRKLDHNCIVRLRYFYSSGKKDEVTNLVDVYBETVYRVARHYSRAKQTLPEVI 166
 |||||Db 115 ELQITRLDHNVAALRHCFSTTE-KDELYNLVLEVPETVYRVARHYSRAKQDMEMI 173
 |||||Qy 167 YVLYMYQLFRSLAYTHSRGICHRDIPKQNLDPDTATLKI CDPSGAQVLRGEPNVSY 226
 |||||Db 174 YVLYMYQLFRSLAYTHSRGICHRDIPKQNLDPDTATLKI CDPSGAQVLRGEPNVSY 233
 |||||Qy 227 ICSRYRABELIFGATDYSSIDVWSAGCVLAELLLGQIPFGDSGVQDLVEIIKVLGTP 286
 |||||Db 234 ICSRYRABELIFGATDYSSIDVWSAGCVLAELLLGQIPFGDSGVQDLVEIIKVLGTP 293
 |||||Qy 287 TREQIRKEMNPNTTEFKPQIKAHPMWKVFRPTPEALACSRLLLEYTPARLTPEACA 346
 |||||Db 294 TREIKSNPNVTEFKPQIKAHPMWKVFRPTPEALACSRLLLEYTPARLTPEACT 353
 |||||Qy 347 HSPFDELDPNVKHPNGRDTPLNFTQEL-SSNPPLATILIPPHAR 393
 |||||Db 354 HSPFDELDPNVKHPNGRDTPLNFTQEL-SSNPPLATILIPPHAR 401
 |||||

RESULT 11

T03601

shaggy protein kinase (EC 2.7.1.1) 6 - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: T03601

R:Takvorian, A.; Schwebel-Dugue, N.; Dornelas, M.C.; Tichindky, G.; Twell, D.; Kreis, M.
 submitted to the EMBL Data Library, October 1996

A:Reference number: 214970

A:Accession: T03601

A:Molecule type: mRNA

A:Residues: 1-471 <TA>

A:Cross-references: UNIPROT:O24139; UNIPARC:UPI00000A7BE6; EMBL:Y08607; P1DN:CAA69899.1

A:Experimental source: cultivar Samsun NN; tissue-type pollen

C:GeneticB:

A:Gene: NSK6

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase; protein kinase

F:140-401/Domain: protein kinase homology <KIN>

Query Match 61.3%; Score 1275.5; DB 2; Length 471;
 Best Local Similarity 61.7%; Pred. No. 7.4e-54;
 Matches 250; Conservative 49; Mismatches 77; Indels 29; Gaps 6;

Qy 11 MSGRPRTTSFASCKPVQGPASFMVSRK-----DSK----- 52

Db 73 MDRPENSEFDE-----LPKEMHEMKIKDEKADSHEDNLEKMPAVVSGNGTGTQITV 126
 |||||Qy 53 T--PGQDPRQEVSYTDTKVIKNGSGFVVYQAKLDSGELVAIKKVLQDGRFKNR 110
 |||||Db 127 TTVSGRNGQQTSTSYAERVVGSGSGIYQAKLETGERVAIKKVLQDGRYKNR 186
 |||||Qy 111 MRKLDHNCIVRLRYFYSSGKKDEVTNLVDVYBETVYRVARHYSRAKQTLPEVIYVYL 170
 |||||Db 187 MRKLDHNCIVRLRYFYSSGKKDEVTNLVDVYBETVYRVARHYSRAKQDMEMIYVYL 245
 |||||

A:Residues: 1-472 <GB>
 A:Cross-references: UNIPROT:Q96287; UNIPARC:UPI000000005A; EMBL:AF058919; NID:93047100;
 C:Genetics:
 A:Gene: ATSP.F6N23.11
 A:Map position: 5
 A:Introns: 21/3; 103/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3; 4
 C:Superfamily: kinase-related transforming protein; protein kinase
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:136-397/Domain: protein kinase homology <KIN>
 F:144-152/Region: protein kinase ATP-binding motif
 F:167/Active site: Lys #status predicted

Query Match 60.5%; Score 1256; DB 1; Length 472;
 Best Local Similarity 61.6%; Pred. No. 5e-53;
 Matches 250; Conservative 54; Mismatches 74; Indels 28; Gaps 9;

Qy 10 GMSGRPTTSPAESCKPV--QPSAFSGSMKV-----SRDKD-----GSKVTTVV 51
 Db 67 GTSNVP-----AVSKRPDDQLPDVMIEKIKIDENANREDKDMETTVVNSGTETGVYI 121
 Qy 52 ATPGGPDRP-QEVSYDTKVIKNGSGGVYQAKLCSGELVAIKVQLQDKRFKRELIQ 109
 Db 122 TTVVGRGDKPKQTISYMAQRVGSGFVGFQAKCLETGEQVAIKVQLQDKRYKREIQ 181
 Qy 110 IMRKLDCNIVRLRYFFYSGSEKDEYVNLVDYVPETVYVARHYSAKQTLPIVYVK 169
 Db 182 IMRLQDHPNVNVLRRSFFSTTD-KDELINLVLEVPETVYVARHYSAKQTLPIVYVK 240
 Qy 170 LYMVQLFSLAYIHS-FGICHRDIKQNLDDPDAVLKLCDFGSAKOLVRGEPNVSYIC 228
 Db 241 LYTVOICALNVYLVHNVGCHRDIKQNLVNPQTHQKICDFGSAKMLVPGEPNISTYC 300
 Qy 229 SRYRABELIFGATDYTSSIDVWSAGCVLAELLGQPIFGSGVDQVLEIKVLGTPTR 288
 Db 301 SRYRABELIFGATEYTNADIMWSGCVLAELLGQPIFGSGVDQVLEIKVLGTPTR 360
 Qy 289 EQIREMNPYTEFKFPQIKAHPMTKVFRPRTPEPAIALCSRLLEYTPARLPLPACAH 348
 Db 361 EIRCMNPYTEFKFPQIKAHPMTKI FHKRMPPEAVDLVSRLLQYSFNLCTALBACAH 420
 Qy 349 FDELDRDPNVKHPNGRDPALFNFPTTOELSSNP-PLATILLIPPHAR 393
 Db 421 FPDLDRLDPNVSLPNGRALPLPFTAQELAGASTELRQRLIPACQ 466

RESULT 15
 S37642
 protein kinase MSK-3 (EC 2.7.1.-) [similarity] - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: S37642
 R:Pay, A.; Jonak, C.; Boegre, L.; Mesiklene, I.; Mairinger, T.; Szalay, A.; Heberle-Bors,
 plant J. 3, 847-856, 1993
 A:Title: The MSK family of alfalfa protein kinase genes encodes homologues of shaggy/15
 A:Reference number: S37642; MUID:94004996; PMID:8401615
 A:Accession: S37642
 A:Molecule type: mRNA
 A:Residues: 1-412 <PAY>
 A:Cross-references: UNIPARC:UPI000016D9F3; EMBL:X68409; NID:g313147; PIDN:CAA48472.1; PI
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:73-334/Domain: protein kinase homology <KIN>
 F:81-89/Region: protein kinase ATP-binding motif
 F:104/Active site: Lys #status predicted

Query Match 60.4%; Score 1256; DB 1; Length 412;
 Best Local Similarity 61.2%; Pred. No. 5e-53;
 Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

Qy 6 MEGGMSGRPTTSPAESCKPV--QPSAFSGSMKVSRDK-----DGSKVTTVV 51
 Db 2 MASGGVA--PASGFIDKASSVGVKLPBEMNDMKIRDDKEMEAATIVDGNGTETGHITV 59

Qy 52 ATPGGPDRP-QEVSYDTKVIKNGSGGVYQAKLCSGELVAIKVQLQDKRFKRELIQ 110
 Db 60 TTIGKNGQPKQTISYMAERVNGSGFVGFQAKCLETGEQVAIKVQLQDKRYKRELIQ 119
 Qy 111 MRKLDCNIVRLRYFFYSGSEKDEYVNLVDYVPETVYVARHYSAKQTLPIVYVK 170
 Db 120 MRLLDHPNVNVLKCFPSTTE-KDELINLVLEVPETVYVARHYSAKQTLPIVYVK 178
 Qy 171 LYMVQLFSLAYIHS-FGICHRDIKQNLDDPDAVLKLCDFGSAKOLVRGEPNVSYIC 229
 Db 179 YSYQICRALAYIHNSIGVCHRDIKQNLVNPQTHQKICDFGSAKMLVPGEPNISTYC 238
 Qy 230 RYRABELIFGATDYTSSIDVWSAGCVLAELLGQPIFGSGVDQVLEIKVLGTPTR 289
 Db 239 RYRABELIFGATEYTNADIMWSAGCVLAELLGQPIFGSGVDQVLEIKVLGTPTR 298
 Qy 290 QIREMNPYTEFKFPQIKAHPMTKVFRPRTPEPAIALCSRLLEYTPARLPLPACAH 349
 Db 299 EIKCMNPYTEFKFPQIKAHPMTKI FHKRMPPEAVDLVSRLLQYSFNLCTALBACAH 358
 Qy 350 FDELDRDPNVKHPNGRDPALFNFPTTOELSSNP-PLATILLIPPHAR 393
 Db 359 YDVRDPTTRLNPGRFLPPLFNVKVELKGVPAEMLVQLVPPHAR 403

Search completed: May 16, 2006, 15:10:18
 Job time : 42 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:02:06 ; Search time 185 Seconds
(without alignments)
935.758 Million cell updates/sec

Title: US-10-689-461-2
Perfect score: 2081
Sequence: 1 MEVPMPEGCGSGRPRRTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	5 ABB07578	ABb07578 Human trn
2	2024	97.3	420	4 AAE05998	AAe05998 Human gly
3	2024	97.3	420	5 ABB07577	ABb07577 Human gly
4	2024	97.3	420	7 ABR44294	ABr44294 Human gly
5	2024	97.3	420	7 ADK11467	ADk11467 Human gly
6	2024	97.3	420	8 ADH09637	ADh09637 Human hos
7	2024	97.3	420	8 ADR40191	ADr40191 Human gly
8	2024	97.3	420	8 ADS92965	ADs92965 Glycogen
9	2024	97.3	420	8 ADT92555	ADt92555 Human gly
10	2013	96.7	414	8 ADR06333	ADr06333 p38-alpha
11	2013	96.7	420	2 AAR61327	AAr61327 Tau-prote
12	2013	96.7	420	5 ABB77875	ABb77875 Amino aci
13	2013	96.7	420	6 ABB70714	ABb70714 Human gly
14	2013	96.7	420	7 ABR44293	ABr44293 Human gly
15	2013	96.7	420	7 ADB68742	ADb68742 Rat tau p
16	2013	96.7	420	8 ADB64053	ADb64053 Human pro
17	2013	96.7	420	8 ADH09634	ADh09634 Human hos
18	2013	96.7	420	8 ADR06320	ADr06320 Gsk-3 bet
19	2013	96.7	420	8 ADR06317	ADr06317 Gsk-3 bet
20	2013	96.7	420	9 ADY64106	ADy64106 Human gly
21	2013	96.7	420	9 AEA39562	AEa39562 Human gly
22	2013	96.7	420	9 AEA39564	AEa39564 Mouse gly
23	2013	96.7	420	9 AEB28124	AEb28124 Human gly
24	2013	96.7	428	7 ADC50594	ADc50594 Human tau

25	2010	96.6	420	2 AAR61326	AAr61326 Tau-prote
26	2010	96.6	420	6 ABR82106	ABr82106 Human gly
27	2010	96.6	420	7 ABR44289	ABr44289 Human gly
28	2010	96.6	420	7 ADE64051	ADe64051 Rat Prote
29	2010	96.6	420	8 ADI28893	ADi28893 Mouse gly
30	1996.5	95.9	433	7 ABR44295	ABr44295 Human gly
31	1996.5	95.9	433	7 ABR44298	ABr44298 Human gly
32	1996.5	95.9	433	7 ADJ69554	ADj69554 Human hea
33	1996.5	95.9	433	8 ADH09633	ADh09633 Human hos
34	1996.5	95.9	433	8 ADO49107	ADo49107 Human ded
35	1996.5	95.9	433	8 ADU20919	ADu20919 Human gly
36	1996.5	95.9	433	8 ADU06409	ADu06409 Novel bro
37	1996.5	95.9	433	9 AEB25735	AEb25735 Human and
38	1996.5	95.9	439	8 ADR66057	ADr66057 Human pro
39	1994.5	95.8	439	8 ADR66399	ADr66399 Human pro
40	1978	95.1	385	9 ADY85481	ADy85481 Catalytic
41	1883.5	90.5	361	5 ABB07579	ABb07579 Human trn
42	1877	90.2	367	8 ADR06334	ADr06334 Gsk-3 bet
43	1877	90.2	378	5 ABB77877	ABb77877 Sequence
44	1872.5	90.0	361	5 ABA47983	ABa47983 Human gly
45	1872.5	90.0	361	7 ADC37107	ADc37107 Human GSK

ALIGNMENTS

RESULT 1	
ABb07578	ABb07578 standard; protein; 394 AA.
AC	ABb07578;
XX	
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human truncated GSK3beta polypeptide 557.
XX	
KW	GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; neurotropic; human;
KW	Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	Peptide
FT	Peptide
FT	Peptide
XX	
PN	MO200210357-A2.
XX	
PD	07-FEB-2002.
XX	
PF	25-JUL-2001; 2001WO-US023539.
XX	
PR	27-JUL-2000; 2000US-0221242P.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY,
PI	Colt DG, Nguyen SH, Medina-Selby A,
XX	
XX	WPI, 2002-188732/24.
DR	
XX	
PT	New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids
PT	encoding them, useful for treating diseases mediated by GSK3 activity,
XX	including Alzheimer's disease, type 2 diabetes and inflammation.
PS	Claim 8; Fig 2A-B; 36pp; English.
XX	
CC	The invention provides glycogen synthase kinase 3 (GSK3) polypeptides
CC	capable of crystallisation, including GSK3alpha and GSK3beta
CC	polypeptides. The GSK polypeptides can be used to identify and optimise
CC	GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as
CC	pharmaceutical agents, for treating diseases mediated by GSK3 activity,

including Alzheimer's disease, type 2 diabetes and inflammation. The
CC present sequence represents the amino acid sequence of a truncated
CC GSK3beta polypeptide 557
XX
SQ Sequence 394 AA;
Query Match 100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 2,7e-216;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEYMPMEGSGMGRPRITTSFAESCKPVQPSAFSGSMKVSXDKSGKTTVVAATPGQGPDR 60
DB 1 MEYMPMEGSGMGRPRITTSFAESCKPVQPSAFSGSMKVSXDKSGKTTVVAATPGQGPDR 60
QY 61 POEVSYDTKVIKNGSGFVVYQAKLDSGELVAIKVLDKRPKNRELQIMRKLDHNCIV 120
DB 61 POEVSYDTKVIKNGSGFVVYQAKLDSGELVAIKVLDKRPKNRELQIMRKLDHNCIV 120
QY 121 RLRFYFSSGSKDEVLNLVDYVPEVTVRAHYSRAKQTLPIYVKLYMYQLFRSLA 180
DB 121 RLRFYFSSGSKDEVLNLVDYVPEVTVRAHYSRAKQTLPIYVKLYMYQLFRSLA 180
QY 181 YHSFGICHRDIKQNLILDDPTAVLKLDFGSAKQIVRGEPNVSYICSRYYRAPELIFG 240
DB 181 YHSFGICHRDIKQNLILDDPTAVLKLDFGSAKQIVRGEPNVSYICSRYYRAPELIFG 240
QY 241 ATDTSSIDWSACVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIREMNPYTE 300
DB 241 ATDTSSIDWSACVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIREMNPYTE 300
QY 301 FKFPQIQAHPWTKVFRRTPPEALALCSRLLEYTPPTARLTPLECAHSFDELDPNVKH 360
DB 301 FKFPQIQAHPWTKVFRRTPPEALALCSRLLEYTPPTARLTPLECAHSFDELDPNVKH 360
QY 361 PNGRDTPALFMTTQELSSNPPLATILIPPHARI 394
DB 361 PNGRDTPALFMTTQELSSNPPLATILIPPHARI 394
RESULT 2
AAE05998 ID AAE05998 standard; protein; 420 AA.
XX
AC AAE05998;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human glycogen synthase kinase 3-beta #1.
XX
KM Antisense: glycogen synthase kinase 3-beta; GSK3B; diabetes; infection;
KM insulin regulation disorder; neurological disorder; Alzheimer's disease;
KM bipolar illness; inflammation; tumour; tau protein kinase I; TPX-1;
KM human.
XX
KW Homo sapiens.
XX
OS
XX
PN MO200152862-A1.
XX
PD 26-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001085.
XX
PR 19-JAN-2000; 2000US-00489765.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Butler MM, McKay R, Monia BP, Wyatt JR;
XX
DR WPI, 2001-457510/49.
XX
DR N-PSDB; AAD11491.
XX
PT Novel antisense compounds, particularly antisense oligonucleotides for
PT inhibiting expression of glycogen synthase kinase 3 beta in cells and for

diagnosing, treating neurological and insulin regulation disorders.
XX
PS Example 13; Page 88-90; 106pp; English.
XX
CC The invention relates to antisense compounds targeted to nucleic acid
CC encoding glycogen synthase kinase 3-beta (GSK3B) (also known as tau
CC protein kinase I (TPK-I)). The antisense compound is useful for
CC inhibiting the expression of glycogen synthase kinase 3-beta enzyme in
CC cells or tissues and for treating diseases or conditions associated with
CC the enzyme such as insulin regulation disorder, in particular diabetes
CC and neurological disorder, e.g. Alzheimer's disease and bipolar illness.
CC The antisense compound is also useful for diagnosing diseases associated
CC with the expression of glycogen synthase kinase 3-beta and for
CC prophylaxis e.g. to prevent or delay infection, inflammation or tumour
CC formation and as a research reagent. The present sequence is human
CC glycogen synthase kinase 3-beta
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPRTTSFAESCKPVQPSAFSGSMKVSXDKSGKTTVVAATPGQGPDRPOEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGSMKVSXDKSGKTTVVAATPGQGPDRPOEVSYDTK 60
QY 71 VINGSGFVVYQAKLDSGELVAIKVLDKRPKNRELQIMRKLDHNCIVRLRFYFYSYG 130
DB 71 VINGSGFVVYQAKLDSGELVAIKVLDKRPKNRELQIMRKLDHNCIVRLRFYFYSYG 120
QY 131 EKKDEVYLNVLVYPEVTVRAHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 190
DB 131 EKKDEVYLNVLVYPEVTVRAHYSRAKQTLPIYVKLYMYQLFRSLAYHSFGICHR 180
QY 191 DIKRONLLDDPTAVLKLDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 250
DB 191 DIKRONLLDDPTAVLKLDFGSAKQIVRGEPNVSYICSRYYRAPELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIREMNPYTEFKFPQIKAMP 310
DB 251 WSAGCVLAELLGQPIFGDSGVQDVEIIVKLGTPPREQIREMNPYTEFKFPQIKAMP 300
QY 311 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLECAHSFDELDPNVKHPNGRDPALF 370
DB 311 WTKVFRPRTPPEALALCSRLLEYTPPTARLTPLECAHSFDELDPNVKHPNGRDPALF 360
QY 371 NFFTQELSSNPPLATILIPPHARI 394
DB 371 NFFTQELSSNPPLATILIPPHARI 384
RESULT 3
ABB07577 ID ABB07577 standard; protein; 420 AA.
XX
AC ABB07577;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human glycogen synthase kinase 3beta (GSK3beta) polypeptide.
XX
KM GSK3; glycogen synthase kinase 3; GSK3alpha; GSK3beta; nootropic; human;
KM Alzheimer's disease; antiinflammatory; antidiabetic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 216
FT Peptide /note= "phosphorylated"
FT Peptide /note= ".419"
FT Peptide /note= "specifically claimed fragment"
FT Peptide 278..419

FT	Peptide	/note= "specifically claimed fragment"
FT	285..384	
FT	/note= "specifically claimed fragment"	
FT	351..384	
FT	Peptide	/note= "specifically claimed fragment"
XX		
XX	WO200210357-A2.	
XX		
XX	07-FEB-2002.	
XX		
XX	25-JUL-2001; 2001WO-US023539.	
XX		
XX	27-JUL-2000; 2000US-0221242P.	
XX		
XX	(CHIR) CHIRON CORP.	
XX		
XX	Harrison SD, Hall JA, Calderon-Cacia M, Zhong Z, Fang EY,	
XX	Cost DG, Nguyen SH, Medina-Selby A;	
XX		
XX	WPI; 2002-188732/24.	
XX		
XX	New glycogen synthase kinase 3 (GSK3) inhibitors and nucleic acids	
XX	encoding them, useful for treating diseases mediated by GSK3 activity,	
XX	including Alzheimer's disease, type 2 diabetes and inflammation.	
XX		
XX	Claim 6; Fig 1A-B; 36pp; English.	
XX		
XX	The invention provides glycogen synthase kinase 3 (GSK3) polypeptides	
XX	capable of crystallization, including GSK3alpha and GSK3beta	
XX	polypeptides. The GSK polypeptides can be used to identify and optimize	
XX	GSK3 inhibitors. Nucleic acid encoding the GSK polypeptides are useful as	
XX	pharmaceutical agents, for treating diseases mediated by GSK3 activity,	
XX	including Alzheimer's disease, type 2 diabetes and inflammation. The	
XX	present sequence represents the amino acid sequence of human GSK3beta	
XX	polypeptide	
XX		
XX	Sequence 420 AA;	
XX		
XX	Query Match	97.3%; Score 2024; DB 5; Length 420;
XX	Best Local Similarity 100.0%; Pred. No. 4.7e-210;	
XX	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	11 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYDTK 70	
DB	1 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYDTK 60	
QY	71 VINGSGFQVNVQAKLCSGSELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 130	
DB	61 VINGSGFQVNVQAKLCSGSELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 120	
QY	131 EKKDEVLTNLVDVVPETVYVARHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 190	
DB	121 EKKDEVLTNLVDVVPETVYVARHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 180	
QY	191 DIKQNLILDDPTAVLKLCDPFGSAKQLYRGEPNNYSICSRYYRABELIFGATDYSIDV 250	
DB	181 DIKQNLILDDPTAVLKLCDPFGSAKQLYRGEPNNYSICSRYYRABELIFGATDYSIDV 240	
QY	251 MSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIRKNNPNYTERKFKFOIKAH 310	
DB	241 MSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIRKNNPNYTERKFKFOIKAH 300	
QY	311 WTKVPRPTPEPAIALCSRLLEYTPARLTPLACAHSPFDELARDPNYCHPNGRDTPALF 370	
DB	301 WTKVPRPTPEPAIALCSRLLEYTPARLTPLACAHSPFDELARDPNYCHPNGRDTPALF 360	
QY	371 NFTTOELSSNPPLATILIPPHARI 394	
DB	361 NFTTOELSSNPPLATILIPPHARI 384	

ID	ABR44294 standard; protein; 420 AA.
XX	
XX	ABR44294;
AC	
XX	
XX	18-AUG-2003 (first entry)
DT	
XX	
XX	Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
DE	
XX	GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
XX	KW GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
XX	KW GSK3; angiogenesis; glycogen synthase kinase-3; antilipemic; cardiant;
XX	vulnerable; antiarteriosclerotic; GSK3beta; enzyme.
XX	
OS	Homo sapiens.
XX	
XX	WO2003038037-A2.
XX	
XX	08-MAY-2003.
XX	
XX	23-OCT-2002; 2002WO-US033909.
XX	
XX	29-OCT-2001; 2001US-0350160P.
XX	
XX	13-NOV-2001; 2001US-0337905P.
XX	
XX	(SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX	
XX	Walsh K;
XX	
XX	WPI; 2003-482140/45.
XX	
XX	Modulating angiogenesis, useful for treating hyperlipidemia, comprises
XX	administering an angiogenesis inhibitor/promoter, such as an
XX	active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3
XX	activator/inhibitor.
XX	
XX	Disclosure; Page 100-101; 115pp; English.
XX	
XX	The invention relates to inhibiting/enhancing angiogenesis. The method
XX	involves administering to a subject needing the treatment, an
XX	angiogenesis inhibitor/promoter, such as an active/inactive glycogen
XX	synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
XX	where the angiogenesis modulator is administered to inhibit/enhance
XX	angiogenesis in a subject. The methods are useful for treating a
XX	condition associated with increased apoptotic cell death of vascular
XX	endothelial cells, where the condition is characterized by lesion of
XX	blood vessel wall, such as hyperlipidemia, also in the treatment of
XX	myocardial infarction and in the promotion of wound healing. The present
XX	sequence represents a human GSK3beta polypeptide (Genbank Accession No.
XX	S53324)
XX	
XX	Sequence 420 AA;
XX	
XX	Query Match
XX	Best Local Similarity 97.3%; Score 2024; DB 7; Length 420;
XX	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	11 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYDTK 70
DB	1 MSGRRPTTSFAESCKPVOQPSAFSGSMKYSRDKDSKVTTVVATPGQGDPRQEVSYDTK 60
QY	71 VINGSGFQVNVQAKLCSGSELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 130
DB	61 VINGSGFQVNVQAKLCSGSELVAIKKVLQDKRFKRELOIMRKLDHCNIVRLRYFFYS 120
QY	131 EKKDEVLTNLVDVVPETVYVARHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 190
DB	121 EKKDEVLTNLVDVVPETVYVARHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSGICHR 180
QY	191 DIKQNLILDDPTAVLKLCDPFGSAKQLYRGEPNNYSICSRYYRABELIFGATDYSIDV 250
DB	181 DIKQNLILDDPTAVLKLCDPFGSAKQLYRGEPNNYSICSRYYRABELIFGATDYSIDV 240
QY	251 MSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIRKNNPNYTERKFKFOIKAH 310
DB	241 MSAGCVLAELLGGPIFPDGSVDQVLEIIVKLGTPTRBOIRKNNPNYTERKFKFOIKAH 300

QY 311 WTKVFRPTPEPALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 370
 DB 301 WTKVFRPTPEPALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 360
 QY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384
 RESULT 5
 ID ADK11467 standard; protein; 420 AA.
 AC ADK11467;
 DE 06-MAY-2004 (first entry)
 DE Human glycogen synthase kinase 3 beta protein.
 KW cytosolic; cardiovascular; immunosuppressive; nephrotoxic;
 KW antirheumatic; antiarthritic; dermatological; antipsoriatic;
 KW antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
 KW cardiovascular disorder; autoimmune disease; glomerulonephritis;
 KW rheumatoid arthritis; dermatological disorder; psoriasis;
 KW inflammatory disorder; malaria; emphysema; alopecia.
 OS Homo sapiens.
 PN MO2003040301-A2.
 PD 15-MAY-2003.
 PE 23-OCT-2002; 2002MO-GB004780.
 PR 05-NOV-2001; 2001GB-00026506.
 PR 27-NOV-2001; 2001GB-00028384.
 PR 11-FEB-2002; 2002GB-00003185.
 PA (CYCL-) CYCLACEL LTD.
 PI Deak P, Frenz L, Glover D, Midgley C;
 DR WPI; 2003-441540/41.
 DR N-PSDB; ADK11466.
 XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,
 PT preventing and/or treating disorders, such as cancer, glomerulonephritis,
 PT rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
 XX Example 27; Page 218; 265pp; English.
 PS The invention relates to novel Drosophila species DNA sequences and their
 XX encoded proteins with their corresponding human homologues. The proteins
 CC or their encoding polynucleotides are useful in a method of prevention,
 CC treatment or diagnosis of a disease in an individual, and used to
 CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC bringing the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide
 CC and/or regulating a cell division cycle function. The diseases also

CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. This sequence represents a human homolog
 CC for one of the Drosophila proteins of the invention.
 XX SQ Sequence 420 AA;
 Query Match 97.3%; Score 2024; DB 7; Length 420;
 Best Local Similarity 100.0%; Pred. No. 4.7e-210;
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSPAESCKPVQSPAFSGMKVSRDKSGKYTTVATPGQSPDRQEVSYTDTK 70
 DB 1 MSGRPRTTSPAESCKPVQSPAFSGMKVSRDKSGKYTTVATPGQSPDRQEVSYTDTK 60
 QY 71 VINGSGFVVYQALCSGSELVAIKKYLQDKRFKRELQIMRKLDHCNIVRLRFFSSG 130
 DB 61 VINGSGFVVYQALCSGSELVAIKKYLQDKRFKRELQIMRKLDHCNIVRLRFFSSG 120
 QY 131 EKKDEVYLNIVLDVVPETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYIHSGICHR 190
 DB 121 EKKDEVYLNIVLDVVPETVYRVARHYSRAKQTLPIVIYKLYMYQLFRSLAYIHSGICHR 180
 QY 191 DIKQNLILDPDITAVLKCDFGSAKQLVRSBPVSYICSRYYRABELIFGATDYSIDV 250
 DB 181 DIKQNLILDPDITAVLKCDFGSAKQLVRSBPVSYICSRYYRABELIFGATDYSIDV 240
 QY 251 WSAGCVIAELLIGQPIPGDSQVDQVEIIVKLTGTPPREQIREMNPVYTEFKFPQIQAMP 310
 DB 241 WSAGCVIAELLIGQPIPGDSQVDQVEIIVKLTGTPPREQIREMNPVYTEFKFPQIQAMP 300
 QY 311 WTKVFRPTPEPALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 370
 DB 301 WTKVFRPTPEPALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPLAF 360
 QY 371 NFTTOELSSNPPLATILIPPHARI 394
 DB 361 NFTTOELSSNPPLATILIPPHARI 384
 RESULT 6
 ADH09637
 ID ADH09637 standard; protein; 420 AA.
 AC ADH09637;
 DE 11-MAR-2004 (first entry)
 DE Human host factor protein, SEQ ID No 165.
 KW antiviral; host factor; retrovirus; HIV; human.
 OS Homo sapiens.
 PN MO2003094847-A2.
 PD 20-NOV-2003.
 PE 07-MAY-2003; 2003MO-US014382.
 PR 07-MAY-2002; 2002US-0378711P.
 PA (UYEM-) UNIV EMORY.
 PI Devine SE;
 DR WPI; 2004-011998/01.
 PT Identifying an antiviral compound useful for treating HIV comprises
 PT exposing a cell that expresses a host factor to a candidate compound to
 PT identify an agent that inhibits the expression or activity of the host
 PT factor.

XX PS Claim 13; SEQ ID NO 165; 141pp; English.
CC The invention relates to a novel method for identifying an antiviral
CC compound. The novel method comprises exposing a cell that expresses a
CC host factor to a candidate compound to identify an agent that inhibits
CC the expression or activity of the host factor. The novel method involves
CC identifying an antiviral compound comprising exposing a first cell that
CC expresses a host factor to a candidate compound, determining whether the
CC candidate compound inhibits the expression or activity of the host factor
CC in the first cell, where a candidate compound that inhibits the
CC expression or activity of the host factor in the first cell is a
CC potential antiviral compound, exposing a second cell to the potential
CC antiviral compound and a retrovirus, and determining whether the compound
CC inhibits the ability of the retrovirus to infect or replicate within the
CC second cell, where a potential antiviral compound that inhibits the
CC ability of the retrovirus to infect the second cell is an antiviral
CC compound. The method is useful in identifying antiviral agents, including
CC those that are effective against retroviruses, such as HIV. This sequence
CC represents a human host factor protein used in the antiviral
CC identification method of the invention.
XX
XX
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRRTTSPAESCKPVOQPSAFSGSMKVSRLDQSGKTTVATPGQGPDRPOEVSYTDK 70
DB 1 MSGRRTTSPAESCKPVOQPSAFSGSMKVSRLDQSGKTTVATPGQGPDRPOEVSYTDK 60
QY 71 VIENGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VIENGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKQDEVYINLVLDVYPEYTVVARRHYSRAKQTLPIYVYKLWYQLFRSLATYHSGICHR 190
DB 121 EKQDEVYINLVLDVYPEYTVVARRHYSRAKQTLPIYVYKLWYQLFRSLATYHSGICHR 180
QY 191 DIKPNLLDPTDPTAVLKLCDFGSAKQLVGSPNVSICSRYYRABELFGATDYSIDV 250
DB 181 DIKPNLLDPTDPTAVLKLCDFGSAKQLVGSPNVSICSRYYRABELFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDQSGVDQVLEIIKVLGTPTRQIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLGQPIFGDQSGVDQVLEIIKVLGTPTRQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVRRPRTPPPAIALCSRLLETPPTARLTPLACAHSPFDELDPNVKGNHGRDTPALF 370
DB 301 WTKVRRPRTPPPAIALCSRLLETPPTARLTPLACAHSPFDELDPNVKGNHGRDTPALF 360
QY 371 NETTOELSSNPPLATILIPPHARI 394
DB 361 NETTOELSSNPPLATILIPPHARI 384
RESULT 7
ID ADR40191 standard; protein; 420 AA.
XX ADR40191;
DT 18-NOV-2004 (first entry)
DE Human glycogen synthase kinase 3 beta (GSK3beta) (1521) protein.
XX haematological; cytosolic; erythroid; anaemia; erythrocytosis;
KM bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;
KM T-cells; neutropenia; gene therapy; human;
XX glycogen synthase kinase 3 beta; GSK3beta; enzyme.
OS Homo sapiens.

XX PN WO2004072242-A2.
XX PD 26-AUG-2004.
XX PF 05-FEB-2004; 2004WO-US003417.
XX 05-FEB-2003; 2003US-0445241P.
PR 18-FEB-2003; 2003US-0448389P.
PR 20-MAR-2003; 2003US-0456320P.
PR 03-APR-2003; 2003US-0460279P.
PR 28-APR-2003; 2003US-0465924P.
PR 13-MAY-2003; 2003US-0470052P.
PR 26-AUG-2003; 2003US-0498106P.
PR 04-SEP-2003; 2003US-0500179P.
PR 15-SEP-2003; 2003US-0502909P.
PR 10-OCT-2003; 2003US-0510351P.
PR 17-OCT-2003; 2003US-0512380P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Kelly LM, Carroll JM, Farlow D, Healy A;
XX WPI; 2004-625850/60.
XX DR N-PESDB; ADR40190.
XX
XX PT Identifying a compound capable of treating a hematological disorder
XX comprises combining a compound to be tested with a polypeptide related
XX PT with the disorder under conditions suitable for binding of the test
XX compound to the polypeptide.
PS Claim 1; SEQ ID NO 72; 321pp; English.
XX
XX The invention relates to a novel method for identifying a compound
XX capable of treating a hematological disorder which comprises combining a
XX compound to be tested with a specific polypeptide under conditions
XX suitable for binding of the test compound to the polypeptide. The method
XX of the invention has hematological and cytostatic applications and may
XX be useful for identifying compounds for treating a hematological
XX disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
XX bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
XX thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
XX identified may be utilized during gene therapy procedures. The current
XX sequence is that of a human haematological disorder-related protein of
XX the invention.
SQ Sequence 420 AA;
Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRRTTSPAESCKPVOQPSAFSGSMKVSRLDQSGKTTVATPGQGPDRPOEVSYTDK 70
DB 1 MSGRRTTSPAESCKPVOQPSAFSGSMKVSRLDQSGKTTVATPGQGPDRPOEVSYTDK 60
QY 71 VIENGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 130
DB 61 VIENGSGFVGVYQAKLCDSGELVAIKVLDKRRFKNRELQIMRKLDHCNIVRLRYFFYS 120
QY 131 EKQDEVYINLVLDVYPEYTVVARRHYSRAKQTLPIYVYKLWYQLFRSLATYHSGICHR 190
DB 121 EKQDEVYINLVLDVYPEYTVVARRHYSRAKQTLPIYVYKLWYQLFRSLATYHSGICHR 180
QY 191 DIKPNLLDPTDPTAVLKLCDFGSAKQLVGSPNVSICSRYYRABELFGATDYSIDV 250
DB 181 DIKPNLLDPTDPTAVLKLCDFGSAKQLVGSPNVSICSRYYRABELFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDQSGVDQVLEIIKVLGTPTRQIREMNPNTTEKFPQIKAH 310
DB 241 WSAGCVLAELLGQPIFGDQSGVDQVLEIIKVLGTPTRQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVRRPRTPPPAIALCSRLLETPPTARLTPLACAHSPFDELDPNVKGNHGRDTPALF 370

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Db      301 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELRDPNVKHPNGRDTPALF 360
Qy      371 NFTTQELSSNPPLATILIPPHARI 394
Db      361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 8
ADSS92965 standard; protein; 420 AA.
XX
AC      ADS92965;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Glycogen synthase kinase 3 beta.
XX
KM      cytostatic; gene therapy; human;
XX      branching morphogenesis modulating agent; MBM agent.
XX
OS      Homo sapiens.
XX
PN      M02004037990-A2.
XX
PD      06-MAY-2004.
XX
PF      22-OCT-2003; 2003MO-US033549.
XX
PR      23-OCT-2002; 2002US-0420554P.
XX      30-DEC-2002; 2002US-0436941P.
XX
PA      (EXBL-) EXELIXIS INC.
XX
PI      Plowman GD, Karim PD, Swimmer C, Haback HA, Koblizek TI,
PI      Schulte-Merker S, Langheinrich U, Stott GM, Trowe T, Vogel AM,
PI      Odenthal JH, Scheel JK, Will TT, Jin Y, Bjerke LM, Hai B,
PI      Adamkiewicz JI, Lickteig K, Hammonds RGR, Amundsen CD, Zhang H;
PI      Nicoll M;
XX
XX      WPI; 2004-365506/34.
XX      N-PSDB; ADS92934.
XX
PT      Identifying a candidate branching morphogenesis modulating agent for
PT      treating cancer comprises contacting the assay system comprising a MBM
PT      polypeptide or nucleic acid with a test agent and detecting a test agent-
PT      biased activity.
XX
PS      Example 3; SEQ ID NO 36; 179pp; English.
XX
CC      The invention describes a method of identifying a candidate branching
CC      morphogenesis modulating (MBM) agent. The method comprises: providing an
CC      assay system comprising a MBM polypeptide or nucleic acid; contacting the
CC      assay system with a test agent under conditions where the system provides
CC      a reference activity, except for the presence of the test agent; and
CC      detecting a test agent-biased activity of the assay system, where a
CC      difference between the test agent-biased activity and the reference
CC      activity identifies the test agent as a candidate branching morphogenesis
CC      modulating agent. Also described are: a method of modulating branching
CC      morphogenesis in a mammalian cell; and a method for diagnosing a disease
CC      in a patient. The method is useful in identifying a candidate branching
CC      morphogenesis modulating agent for preparing a composition for diagnosing
CC      or treating cancer. This is the amino acid sequence of a human branching
CC      morphogenesis modulating (MBM) protein.
XX
SQ      Sequence 420 AA;
XX
Query March 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. NO. 4.7e-210;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      11 MSGRPRTTSFAESCCKPVQGPSAFGSMKVSRLKDSKVTTVVATPGQGPDRPQEVSYDTTK 70
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Db      1 MSGRPRTTSFAESCCKPVQGPSAFGSMKVSRLKDSKVTTVVATPGQGPDRPQEVSYDTTK 60
Qy      71 VINGSGFVYVQATLCSGSELVAIKYLODKRFKNRELQIMRKLDHGNIVRLRYEFPSSG 130
Db      61 VINGSGFVYVQATLCSGSELVAIKYLODKRFKNRELQIMRKLDHGNIVRLRYEFPSSG 120
Qy      131 EKDEYVLNLVLDVVPETVVRVAHYSRAKQTLPIIVKLYMYQLFRSLAYIHSFGICHR 190
Db      121 EKDEYVLNLVLDVVPETVVRVAHYSRAKQTLPIIVKLYMYQLFRSLAYIHSFGICHR 180
Qy      191 DIFQNLILDPDPAVLKLCDFGSAKQLVKGBPNVSYICSRYYRABELIFGATDYSIDV 250
Db      181 DIFQNLILDPDPAVLKLCDFGSAKQLVKGBPNVSYICSRYYRABELIFGATDYSIDV 240
Qy      251 MSAGCVLAEILLGQPIFGPSGVQDLVEIIKVLTGTPPREQIRENNPYTERKPKQIRAKHP 310
Db      241 MSAGCVLAEILLGQPIFGPSGVQDLVEIIKVLTGTPPREQIRENNPYTERKPKQIRAKHP 300
Qy      311 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELRDPNVKHPNGRDTPALF 370
Db      301 WTKVFRPRTPEALALCSRLLEYTPARLTPLBACAHSPFDELRDPNVKHPNGRDTPALF 360
Qy      371 NFTTQELSSNPPLATILIPPHARI 394
Db      361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 9
ADT92555 standard; protein; 420 AA.
XX
AC      ADT92555;
XX
DT      13-JAN-2005 (first entry)
XX
DE      Human glycogen synthase kinase-3-related protein - SEQ ID 1.
XX
KM      neurodegenerative drug; glycogen synthase kinase-3;
XX      neurological disease; Parkinson's disease; Alzheimer's disease;
XX      Down's syndrome; cerebrovascular accident; stroke; spinal injury;
XX      Huntington's chorea; multiple sclerosis; amyotrophic lateral sclerosis;
XX      epilepsy; anxiety disorder; schizophrenia; depression;
XX      manic-depressive psychosis.
XX
OS      Homo sapiens.
XX
PN      M02004091663-A1.
XX
PD      28-OCT-2004.
XX
PF      16-APR-2004; 2004MO-JP005503.
XX
PR      18-APR-2003; 2003JP-00114579.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Morishita T, Sakurada K, Suzuki K, Ikeda S;
XX      WPI; 2004-784511/77.
XX      N-PSDB; ADT92556.
XX
PT      Neurodegenerative drug for treating neurological disease e.g. Parkinson's
PT      disease, Alzheimer's disease and Down's syndrome, contains substance
PT      which inhibits activity of glycogen synthase kinase-3 as active
PT      ingredient.
XX
PS      Disclosure; SEQ ID NO 1; 115pp; Japanese.
XX
CC      The invention comprises a neurodegenerative drug that inhibits the
CC      activity of glycogen synthase kinase-3 (GSK-3). The neurodegenerative
CC      drug of the invention is useful for treating neurological disease, such
CC      as: Parkinson's disease, Alzheimer's disease, Down's syndrome,
CC      cerebrovascular accident, stroke, spinal injury, Huntington's chorea,

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multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, anxiety disorder, schizophrenia, depression and manic-depressive psychosis. The present human protein is used in the exemplification of the invention.

Sequence 420 AA;

Query Match 97.3%; Score 2024; DB 8; Length 420;

Best Local Similarity 100.0%; Pred. No. 4.7e-210; Indels 0; Gaps 0;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGPDRPOEVSYTDTK 70
DB 1 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGPDRPOEVSYTDTK 60
QY 71 VINGSGFGVYVQAKLCDSGELVAIKKVLQDKRFKRELIQMKLDHCNIVLRFFYSYG 130
DB 61 VINGSGFGVYVQAKLCDSGELVAIKKVLQDKRFKRELIQMKLDHCNIVLRFFYSYG 120
QY 131 EKKDEVYINLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYIHSFGICHR 190
DB 121 EKKDEVYINLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYIHSFGICHR 180
QY 191 DIKPNLLDPTAVLKLCDFGSAKQVKGEPNVSICSRYYRABELIFGATDYTSIDV 250
DB 181 DIKPNLLDPTAVLKLCDFGSAKQVKGEPNVSICSRYYRABELIFGATDYTSIDV 240
QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRRQIREMNPNTTEKFPQIKAH 310
DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRRQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPPPEALALCSRLLEYTPARLTPLACAHSPFDLRDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPPPEALALCSRLLEYTPARLTPLACAHSPFDLRDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
```

RESULT 10

ADRO6333 standard; protein; 414 AA.

ID ADRO6333;

AC ADRO6333;

DT 07-OCT-2004 (first entry)

DE p38-alpha kinase, SEQ ID 31.

XX Switch control ligand; switch control pocket;

KW protein activity modulation; human; p38-alpha kinase; enzyme.

XX Homo sapiens.

XX WO2004061084-A2.

XX 22-JUL-2004.

XX 26-DEC-2003; 2003WO-US041450.

XX 31-DEC-2002; 2002US-0437304P.

XX 31-DEC-2002; 2002US-0437403P.

XX 31-DEC-2002; 2002US-0437415P.

XX 18-APR-2003; 2003US-0463804P.

XX 24-DEC-2003; 53US-00463804.

XX (DECI-) DECIPHERA PHARM INC.

XX Flynn DL, Petrillo PA;

XX WPI; 2004-534376/51.

PT Identifying molecules that interact with specific naturally occurring proteins for modulating protein activity, comprises identifying molecules that bind with the protein at the region of the pocket to regulate activity of the protein.

XX Disclosure; SEQ ID NO 31; 204pp; English.

CC The present invention relates to a method for identifying molecules, which interact with proteins e.g. enzymes, receptors, or signaling proteins, in order to regulate the activity of the proteins. The method comprises: identifying a switch control ligand forming a part of the protein; identifying a switch control pocket forming a part of the protein; and which interacts with the switch control ligand, where the ligand interacting in vivo with the pocket to regulate the conformation and biological activity of the protein so that the protein will assume a first conformation and a first biological activity upon the ligand-pocket interaction, and will assume a second, different conformation and a biological activity in the absence of the ligand-pocket interaction; providing respective samples of the protein in the first and second conformations; and screening at least one of the samples against one or more candidate molecules by contacting the molecules and one sample, and identifying small molecules which bind with the protein at the region of the pocket in order to regulate the activity of the protein. The method is useful for modulating protein activity and for the identification of new pharmacological compounds and for treatment modalities. The present sequence is p38-alpha kinase for which a switch control ligand was produced.

CC Sequence 414 AA;

Query Match 96.7%; Score 2013; DB 8; Length 414;

Best Local Similarity 99.7%; Pred. No. 7.2e-209; Indels 0; Gaps 0;

Matches 383; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
QY 11 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGPDRPOEVSYTDTK 70
DB 1 MSGRPRITTSFAESCKPVOQPSAFSGMKVSRDQSGSKYTTVATPGQGPDRPOEVSYTDTK 60
QY 71 VINGSGFGVYVQAKLCDSGELVAIKKVLQDKRFKRELIQMKLDHCNIVLRFFYSYG 130
DB 61 VINGSGFGVYVQAKLCDSGELVAIKKVLQDKRFKRELIQMKLDHCNIVLRFFYSYG 120
QY 131 EKKDEVYINLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYIHSFGICHR 190
DB 121 EKKDEVYINLVLDVPEYTVVARRHYSRAKOTLPVIYVKLYMYOLFRLSLAYIHSFGICHR 180
QY 191 DIKPNLLDPTAVLKLCDFGSAKQVKGEPNVSICSRYYRABELIFGATDYTSIDV 250
DB 181 DIKPNLLDPTAVLKLCDFGSAKQVKGEPNVSICSRYYRABELIFGATDYTSIDV 240
QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRRQIREMNPNTTEKFPQIKAH 310
DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRRQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPRTPPPEALALCSRLLEYTPARLTPLACAHSPFDLRDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPPPEALALCSRLLEYTPARLTPLACAHSPFDLRDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
```

RESULT 11

AAR61327 standard; protein; 420 AA.

ID AAR61327;

AC AAR61327;

DT 25-MAR-2003 (revised)

DT 21-APR-1995 (first entry)

XX Tau-protein kinase I (TPK-I), Alzheimer's disease.

XX Tau-protein kinase I enzyme; TPK-I; Alzheimer's disease.
KM Ractus ractus.
OS EPE16032-A2.
XX 21-SEP-1994.
PD 01-MAR-1994; 94EP-00103057.
XX 02-MAR-1993; 93JP-00041160.
XX 22-MAR-1993; 93JP-00085143.
PR 02-AUG-1993; 93JP-00191246.
XX (MITU) MITSUBISHI KASEI CORP.
PA (MITU) MITSUBISHI CHEM CORP.
XX Takashima A, Hoshino T, Imahori K, Saito K, Shiratsuchi A,
PI Sato S;
XX WPI; 1994-287181/36.
DR N-PSDB; AA067459.
XX Newly isolated tau-protein kinase I enzyme - with specificity for tau-
PT protein providing means for prevention and treatment of Alzheimer's
PT disease.
XX Claim 4; Page 18; 30pp; English.
XX AA067459 codes for a newly isolated tau-protein kinase I enzyme ('TPK-I'),
CC shown in AAR61327 (compare to human AAR61326). The cDNA was cloned from a
CC rat fetus brain cDNA library, and was expressed in insect cells. TPK-I
CC acts specifically on tau-protein, which is thought to be involved in
CC Alzheimer's disease (AD) and senile dementia of the AD type. It is hoped
CC that the characterization of TPK-I may lead to development of new agents
CC for the prevention and therapy of these diseases. (Updated on 25-MAR-2003
CC to correct PW field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 420 AA;
Query Match 96.7%; Score 2013; DB 2; Length 420;
Best Local Similarity 99.7%; Pred. No. 7,4e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 MSGRPRTTSPAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRTTSPAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 120
QY 131 EKKDEVYLNVLVDVPEVTVRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYLNVLVDVPEVTVRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 180
QY 191 DIKQONLLDPTDAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYSIDV 250
DB 181 DIKQONLLDPTDAVLKLCDFGSAKQLVGEPNVSYICSRYYRABELIFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFFGDSGVQDLVAILIVLGTPTREQIREMNPNTTEKFPQIKRHP 310
DB 241 WSAGCVLAELLGQPIFFGDSGVQDLVAILIVLGTPTREQIREMNPNTTEKFPQIKRHP 300
QY 311 WTKKFRPTPEALATLCSRLLEYTPARLTPLEACAHSEFDELKDPNVKHNKGRDTPALF 370
DB 301 WTKKFRPTPEALATLCSRLLEYTPARLTPLEACAHSEFDELKDPNVKHNKGRDTPALF 360
QY 371 NFFTOELSSNPPLATILIPPHARI 394
DB 361 NFFTOELSSNPPLATILIPPHARI 384

RESULT 12
ABR77875
ID ABR77875 standard; peptide; 420 AA.
XX
XX ABR77875;
AC
XX 27-SEP-2002 (first entry)
DT
XX Amino acid sequence of glycogen synthase kinase 3 isoform beta.
DE
XX Glycogen synthase kinase 3 beta; GSK3beta; T-cell lymphoma; stroke;
XX Type II diabetes mellitus; obesity; neurodegenerative disorder; cancer;
KM Alzheimer's disease; mood disorder; depression; schizophrenia;
KM cyclin-dependent kinase 2; substrate; protein coordinate data.
XX
XX Homo sapiens.
OS
XX WO200250254-A2.
PN
XX 27-JUN-2002.
PD
XX 18-DEC-2001; 2001WO-GB005632.
PF
XX 18-DEC-2000; 2000GB-00030846.
PR 14-AUG-2001; 2001GB-00019796.
XX 18-DEC-2000; 2000GB-00030846.
PR 14-AUG-2001; 2001GB-00019796.
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA
PI Bax B, Brown M, Reith A;
XX WPI; 2002-519885/55.
DR
XX Novel crystal structures comprising glycogen synthase kinase (GSK)-3 beta
PT protein or crystal structure comprising a GSK-3 beta: frequently
PT rearranged in advanced T-cell lymphomas (RRAT)-tide complex in
PT crystalline form.
XX
XX Claim 6; Page 23; 327pp; English.
PS
XX The specification describes the structure of glycogen synthase kinase
CC (GSK)3beta protein in crystalline form. GSK3beta is frequently rearranged
CC in advanced T-cell lymphomas. The crystalline structure of GSK3beta is
CC useful in the design or selection of potential inhibitors and/or
CC activators of GSK3beta kinase activity. Such inhibitors and activators
CC are useful for treating Type II diabetes mellitus, obesity,
CC neurodegenerative disorders such as Alzheimer's disease, stroke and mood
CC disorders such as bipolar and unipolar depression, schizophrenia, cancer,
CC in humans. Because GSK3beta may crystallize in more than one crystal
CC form, the structure coordinates of GSK3 or its portions are particularly
CC useful to solve the structure of other crystal forms of GSK3. They may
CC also be used to solve the structure of GSK3 mutants, GSK3 co-complexes,
CC or of the crystalline form of any other protein, particularly kinases
CC with significant amino acid sequence homology to any functional domain of
CC GSK3. The present sequence represents the beta isoform of GSK3, GSK3beta
XX
SQ Sequence 420 AA;
Query Match 96.7%; Score 2013; DB 5; Length 420;
Best Local Similarity 99.7%; Pred. No. 7,4e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 MSGRPRTTSPAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRTTSPAESCKPVQPSAFSGMKVSRDKGSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLDCSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 130
DB 61 VINGSGFVVYQAKLDCSGELVAIKKYLQDKRFKRELOIRKLDHCNIVRLRYFFSSG 120
QY 131 EKKDEVYLNVLVDVPEVTVRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKKDEVYLNVLVDVPEVTVRVARHYSRAKQTLPIVIYVKLYMYQLFRSLAYIHSFGICHR 180

QY 191 DIKPNLLDPDTAVLKLCDPSAKQIVRGEPNVSICSRYYRAPELIFGATDYSIDV 250
 DB 181 DIKPNLLDPDTAVLKLCDPSAKQIVRGEPNVSICSRYYRAPELIFGATDYSIDV 240
 QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPNTTEKFPQIKAH 310
 DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPNTTEKFPQIKAH 300
 QY 311 WTKVFRPPTPEPAIALCSRLLLEYTPPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPPTPEPAIALCSRLLLEYTPPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 360
 QY 371 NPTTOELSSNPPLATILIPPHARI 394
 DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 13
 ABP70714
 ID ABP70714 standard; protein; 420 AA.
 AC ABP70714;
 XX 22-APR-2003 (first entry)
 DT
 XX Human glycogen synthase kinase-3 beta.
 DE Human glycogen synthase kinase-3 beta; protein co-ordinate data;
 KW Human; enzyme; glycogen synthase kinase-3 beta; protein co-ordinate data;
 KW noctropic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;
 KW antiinflammatory; cardiovascular; antiallergic; antiaesthetic; GSK-3;
 KW antiparkinsonian; anticonvulsant; dermatological; vasotropic; GSK-3;
 KW schizophrénia; Alzheimer's disease; diabetes; autoimmune disease;
 KW inflammatory disease; metabolic; neurological; neurodegenerative;
 KW cardiovascular disease; allergy; asthma; Huntington's disease;
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;
 KW amyotrophic lateral sclerosis; multiple sclerosis; kinase;
 KW cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.
 KM
 XX Homo sapiens.
 OS
 XX MO200288078-A2.
 PN
 XX 07-NOV-2002.
 PD
 XX 29-APR-2002; 2002MO-US013511.
 PF
 XX 30-APR-2001; 2001US-0287366P.
 PR 08-JUN-2001; 2001US-0297094P.
 PR 27-FEB-2002; 2002US-0361899P.
 PR
 XX (VERT-) VERTEX PHARM INC.
 PA
 XX Ter Haar E, Swenson L, Green J, Arnott MJ;
 PI
 XX WPI; 2003-247844/24.
 DR
 XX New pyrazolo(3,4-c)pyridazine derivatives are glucogen synthase kinase -3
 PT inhibitor useful for treating e.g. schizophrenia, Alzheimer's disease,
 PT diabetes, autoimmune diseases, allergy, asthma, multiple sclerosis, and
 PT baldness.
 PT
 XX Claim 36; Page 777-778; 778BP; English.
 XX
 CC The present invention relates to novel pyrazolo(3,4-c)pyridazine
 CC derivatives, which have glucogen synthase kinase-3 (GSK-3) inhibitory
 CC activity. The derivatives are useful for inhibiting beta-catenin
 CC phosphorylation and hyperphosphorylated Tau protein production in a
 CC patient and GSK-3 activity in a patient or in a biological sample. The
 CC derivatives are also useful for treating schizophrenia, Alzheimer's
 CC disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,
 CC neurological and neurodegenerative diseases, cardiovascular diseases,
 CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related

CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.
 CC The present sequence is human GSK-3 beta, used to illustrate the
 CC invention. GSK-3 beta is a serine/threonine protein kinase
 CC
 XX
 SQ Sequence 420 AA;
 Query Match 96.7%; Score 2013; DB 6; Length 420;
 Best Local Similarity 99.7%; Pred. No. 7,4e-209;
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 11 MSGRPRTTSFASCKPVOQPSAFSGMKYSRDKDGSKTTVVATPQGGPDEVSYYDTK 70
 DB 1 MSGRPRTTSFASCKPVOQPSAFSGMKYSRDKDGSKTTVVATPQGGPDEVSYYDTK 60
 QY 71 VINGSGFCVVYQAKLDCSGELVAIKVQLDQRFPKRELQIRKLDHCNIVLRIFYSSG 130
 DB 61 VINGSGFCVVYQAKLDCSGELVAIKVQLDQRFPKRELQIRKLDHCNIVLRIFYSSG 120
 QY 131 EKQBEVYINLVLDVPEVTVVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSFGICHR 190
 DB 121 EKQBEVYINLVLDVPEVTVVVAHYSRAKQTLPIYVYKLYMYQLFRSLAYIHSFGICHR 180
 QY 191 DIKPNLLDPDTAVLKLCDPSAKQIVRGEPNVSICSRYYRAPELIFGATDYSIDV 250
 DB 181 DIKPNLLDPDTAVLKLCDPSAKQIVRGEPNVSICSRYYRAPELIFGATDYSIDV 240
 QY 251 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPNTTEKFPQIKAH 310
 DB 241 MSAGCVLAELLGQPIFPDGSVDQVLEIKVLGTPTRQIREMNPNTTEKFPQIKAH 300
 QY 311 WTKVFRPPTPEPAIALCSRLLLEYTPPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 370
 DB 301 WTKVFRPPTPEPAIALCSRLLLEYTPPTARLTPLEACAHSPFDELRDPNVKHPNGRDTPALF 360
 QY 371 NPTTOELSSNPPLATILIPPHARI 394
 DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 14
 ABR44293
 ID ABR44293 standard; protein; 420 AA.
 AC ABR44293;
 XX 18-AUG-2003 (first entry)
 DT
 XX Human glycogen synthase kinase-3 (GSK3)beta polypeptide.
 DE
 XX GSK3; angiogenesis; glycogen synthase kinase-3; antidiabetic; cardiant;
 KW KW vulnery; antiarteriosclerotic; GSK3beta; enzyme.
 KM
 XX Homo sapiens.
 OS
 XX MO2003038037-A2.
 PN
 XX 08-MAY-2003.
 PD
 XX 23-OCT-2002; 2002MO-US033909.
 PF
 XX 29-OCT-2001; 2001US-0350160P.
 PR 13-NOV-2001; 2001US-0337905P.
 PR
 XX (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
 PA
 XX Walsh K;
 PI
 XX WPI; 2003-482140/45.
 DR
 XX Modulating angiogenesis, useful for treating hyperlipidemia, comprises
 PT administering an angiogenesis inhibitor/promoter, such as an
 PT active/inactive glycogen synthase kinase-3 (GSK3) molecule or a GSK3

PT activator/inhibitor.
XX
PS Disclosure; Page 97-99; 115pp; English.
XX
CC The invention relates to inhibiting/enhancing angiogenesis. The method
XX involves administering to a subject needing the treatment, an
CC angiogenesis inhibitor/promoter, such as an active/inactive glycogen
CC synthase kinase-3 (GSK3) molecule or a GSK3 kinase activator/inhibitor,
CC where the angiogenesis modulator is administered to inhibit/enhance
CC angiogenesis in a subject. The methods are useful for treating a
CC condition associated with increased apoptotic cell death of vascular
CC endothelial cells, where the condition is characterized by lesion of
CC blood vessel wall, such as hyperlipidemia, also in the treatment of
CC myocardial infarction and in the promotion of wound healing. The present
CC sequence represents a human GSK3beta polypeptide (GenBank Accession No.
CC P49841)
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.4e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGGVVYQAKLDSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSSG 130
DB 61 VINGSGGVVYQAKLDSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVYVKLYMQQLFRSLAYIHSGFICHR 190
DB 121 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVYVKLYMQQLFRSLAYIHSGFICHR 180
QY 191 DIRQNLILDPDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRAPELLFGATDYSIDV 250
DB 181 DIRQNLILDPDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRAPELLFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLGTPTRREQIREMNPVYTEFKFPQIKAMP 310
DB 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLGTPTRREQIREMNPVYTEFKFPQIKAMP 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 15
ADD68742
ID ADD68742 standard; protein; 420 AA.
XX
AC ADD68742;
XX
DT 15-JAN-2004 (first entry)
XX
DE Rat tau phosphorylation-related protein.
XX
KW tau; phosphoenzyme I; Alzheimer's disease; senile dementia;
KW berline-threonine phosphorylation; rac.
XX
OS Rattus sp.
XX
PN JP2002335983-A.
XX
PD 26-NOV-2002.
XX
PF 03-JUL-1992; 2002JP-00129146.
XX

PR 03-JUL-1992; 92JP-00177241.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 2003-460769/44.
XX
PT N-PSDB; ADD68695.
XX
PS Phosphorylation of tau protein.
XX
PS Disclosure; Page 11-13; 23pp; Japanese.
XX
CC The invention relates to a novel method for the phosphorylation of tau
CC protein in which tau protein or its partial peptide is phosphorylated by
CC the action of phosphoenzyme I, a serine-threonine phospholase. The
CC method of the invention may be used for elucidation of the cause of
CC Alzheimer's disease and Alzheimer type senile dementia. The current
CC sequence is that of the rat tau phosphorylation-related protein of the
CC invention.
XX
SQ Sequence 420 AA;

Query Match 96.7%; Score 2013; DB 7; Length 420;
Best Local Similarity 99.7%; Pred. No. 7.4e-209;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFGSMKVSRLDKGSKVTTVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGGVVYQAKLDSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSSG 130
DB 61 VINGSGGVVYQAKLDSGSELVAIKVLDKRFKRELQIMRKLDHCNIVRLRYFFYSSG 120
QY 131 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVYVKLYMQQLFRSLAYIHSGFICHR 190
DB 121 EKQDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVYVKLYMQQLFRSLAYIHSGFICHR 180
QY 191 DIRQNLILDPDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRAPELLFGATDYSIDV 250
DB 181 DIRQNLILDPDPTAVLKLCDFGSAKQVLRGEPNVSYICSRYYRAPELLFGATDYSIDV 240
QY 251 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLGTPTRREQIREMNPVYTEFKFPQIKAMP 310
DB 241 WSAGCVLAELLGQPIFGDSGVQDLVEIIVKLGTPTRREQIREMNPVYTEFKFPQIKAMP 300
QY 311 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDPALF 370
DB 301 WTKVFRPRTPEPAIALCSRLLEYTPPTARLTPLEACAHSPFDELDPNVKHPNGRDPALF 360
QY 371 NFTTQELSSNPPLATILIPPHARI 394
DB 361 NFTTQELSSNPPLATILIPPHARI 384

Search completed: May 16, 2006, 15:05:37
Job time : 187 secs

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OM protein - protein search, using sw model

Run on: May 16, 2006, 15:20:57 ; Search time 167 Seconds
(without alignments)
985.777 Million cell updates/sec

Title: US-10-689-461-2

Perfect score: 2081

Sequence: 1 MEYPMMEGSGSGRPRTTSF.....OELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2081	100.0	394	3	US-09-916-109-2
2	2081	100.0	394	4	US-10-211-412A-2
3	2081	100.0	394	5	US-10-689-461-2
4	2024	97.3	420	3	US-09-916-109-1
5	2024	97.3	420	4	US-10-211-412A-1
6	2024	97.3	420	5	US-10-278-759-7
7	2024	97.3	420	5	US-10-482-532-4
8	2024	97.3	420	5	US-10-772-632-72
9	2024	97.3	420	5	US-10-689-461-1
10	2024	97.3	420	5	US-10-840-060-257
11	2013	96.7	414	4	US-10-746-545-31
12	2013	96.7	420	4	US-10-278-759-6
13	2013	96.7	420	4	US-10-135-255-1
14	2013	96.7	420	4	US-10-746-545-15
15	2013	96.7	420	4	US-10-746-545-18
16	2010	96.6	420	4	US-10-278-759-2
17	2010	96.6	420	4	US-10-322-153A-1
18	2010	96.6	420	4	US-10-613-728-8
19	1997	96.0	385	4	US-10-664-421-53
20	1997	96.0	385	5	US-10-941-635-53
21	1996.5	95.9	433	4	US-10-278-759-8
22	1996.5	95.9	433	4	US-10-278-759-14
23	1996.5	95.9	433	4	US-10-302-812-62
24	1996.5	95.9	433	4	US-10-408-765A-1360
25	1996.5	95.9	433	5	US-10-828-669-5
26	1883.5	90.5	361	3	US-09-916-109-3
27	1883.5	90.5	361	4	US-10-211-412A-3

28	1883.5	90.5	361	5	US-10-689-461-3	Sequence 3, Appl1
29	1877	90.2	367	4	US-10-746-545-32	Sequence 32, Appl1
30	1872.5	90.0	361	4	US-10-450-422-1	Sequence 1, Appl1
31	1817	87.3	352	4	US-10-664-421-31	Sequence 11, Appl1
32	1817	87.3	352	4	US-10-746-545-16	Sequence 16, Appl1
33	1817	87.3	352	4	US-10-746-545-17	Sequence 17, Appl1
34	1817	87.3	352	5	US-10-941-635-11	Sequence 31, Appl1
35	1817	87.3	352	6	US-11-021-951-167	Sequence 167, App
36	1803	86.6	350	4	US-10-746-545-27	Sequence 27, Appl1
37	1666.5	80.1	407	5	US-10-732-923-1457	Sequence 1457, Ap
38	1634.5	78.5	428	5	US-10-491-467-13	Sequence 13, Appl1
39	1609	77.3	447	3	US-09-916-109-5	Sequence 5, Appl1
40	1609	77.3	447	4	US-10-211-412A-5	Sequence 5, Appl1
41	1609	77.3	447	5	US-10-689-461-5	Sequence 5, Appl1
42	1609	77.3	483	3	US-09-916-109-4	Sequence 4, Appl1
43	1609	77.3	483	4	US-10-211-412A-4	Sequence 4, Appl1
44	1609	77.3	483	4	US-10-278-759-3	Sequence 3, Appl1
45	1609	77.3	483	4	US-10-278-759-4	Sequence 4, Appl1

ALIGNMENTS

```
RESULT 1
US-09-916-109-2
; Sequence 2, Application US/09916109
; Patent No. US20020082408A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacela, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916.109
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-916-109-2
Query Match 100.0%; Score 2081; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.3e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEYPMMEGSGSGRPRTTSFASCKPVOQPSAFSGMKVSRDQSGKTTVVATPGQFDR 60
1 MEYPMMEGSGSGRPRTTSFASCKPVOQPSAFSGMKVSRDQSGKTTVVATPGQFDR 60
Db 1 MEYPMMEGSGSGRPRTTSFASCKPVOQPSAFSGMKVSRDQSGKTTVVATPGQFDR 60
QY 61 POEVSYTDTKVINGSGFVVYQAKLCDGSELVAIKVQLDRKFKXRELQWRKLDHCNIV 120
61 POEVSYTDTKVINGSGFVVYQAKLCDGSELVAIKVQLDRKFKXRELQWRKLDHCNIV 120
Db 61 POEVSYTDTKVINGSGFVVYQAKLCDGSELVAIKVQLDRKFKXRELQWRKLDHCNIV 120
QY 121 RLRFPPYSSGKQKQEVYINLVLDYVPETVYVVAHYSKAKOTLPITYIKLWYOLFSLA 180
121 RLRFPPYSSGKQKQEVYINLVLDYVPETVYVVAHYSKAKOTLPITYIKLWYOLFSLA 180
Db 121 RLRFPPYSSGKQKQEVYINLVLDYVPETVYVVAHYSKAKOTLPITYIKLWYOLFSLA 180
QY 181 YHSFGICHRDIKQNLDDPTAVLKLCDGSAKQVGRGPNYSYICRRYRABELIFG 240
181 YHSFGICHRDIKQNLDDPTAVLKLCDGSAKQVGRGPNYSYICRRYRABELIFG 240
Db 181 YHSFGICHRDIKQNLDDPTAVLKLCDGSAKQVGRGPNYSYICRRYRABELIFG 240
QY 241 ATDYTSIDVWSAGCVLAELLGGPIFGDGVQLVEIIVLGTPTREQIREMNPYTE 300
241 ATDYTSIDVWSAGCVLAELLGGPIFGDGVQLVEIIVLGTPTREQIREMNPYTE 300
Db 241 ATDYTSIDVWSAGCVLAELLGGPIFGDGVQLVEIIVLGTPTREQIREMNPYTE 300
QY 301 FKFOIKAHPTKVPFRPTPEALALCSRLLETPYTAULTFLBACNHSFPDELDPNVKH 360
301 FKFOIKAHPTKVPFRPTPEALALCSRLLETPYTAULTFLBACNHSFPDELDPNVKH 360
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Db      301 FKFPQIAHPWTQVFRPRTPEAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
        |||
Qy      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394
        |||
Db      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394

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RESULT 2

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US-10-211-412A-2
; Sequence 2, Application US/10211412A
; Publication No. US2003007798A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.004/200130.524D1
; CURRENT APPLICATION NUMBER: US/10/211.412A
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-412A-2

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Query Match      100.0%; Score 2081; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.3e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEYPMEGGMSGRPRTTFAESCKPVQPSAFSGMKVSRDKSGKTTVATPGGQDR 60
        |||
Db      1 MEYPMEGGMSGRPRTTFAESCKPVQPSAFSGMKVSRDKSGKTTVATPGGQDR 60
        |||
Qy      61 POEVSYDTKVIKNGSGFVYVYQAKLDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
        |||
Db      61 POEVSYDTKVIKNGSGFVYVYQAKLDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
        |||
Qy      121 RLRYFFYSSEKDEVTYLVLDYVPEVTVRVARHYSRAKOTLPVIYVKLYMQLFRSLA 180
        |||
Db      121 RLRYFFYSSEKDEVTYLVLDYVPEVTVRVARHYSRAKOTLPVIYVKLYMQLFRSLA 180
        |||
Qy      181 YIHSFGICHRDIPQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFG 240
        |||
Db      181 YIHSFGICHRDIPQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFG 240
        |||
Qy      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPREQIRENNPYTE 300
        |||
Db      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPREQIRENNPYTE 300
        |||
Qy      301 FKFPQIAHPWTQVFRPRTPEAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
        |||
Db      301 FKFPQIAHPWTQVFRPRTPEAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
        |||
Qy      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394
        |||
Db      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394

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RESULT 3

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US-10-689-461-2
; Sequence 2, Application US/10689461
; Publication No. US2005004851A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.

```

```

; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/689,461
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-461-2

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Query Match      100.0%; Score 2081; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 3.3e-169;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEYPMEGGMSGRPRTTFAESCKPVQPSAFSGMKVSRDKSGKTTVATPGGQDR 60
        |||
Db      1 MEYPMEGGMSGRPRTTFAESCKPVQPSAFSGMKVSRDKSGKTTVATPGGQDR 60
        |||
Qy      61 POEVSYDTKVIKNGSGFVYVYQAKLDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
        |||
Db      61 POEVSYDTKVIKNGSGFVYVYQAKLDSGELVAIKVLDQKRFNRELQIMRKLDHCNIY 120
        |||
Qy      121 RLRYFFYSSEKDEVTYLVLDYVPEVTVRVARHYSRAKOTLPVIYVKLYMQLFRSLA 180
        |||
Db      121 RLRYFFYSSEKDEVTYLVLDYVPEVTVRVARHYSRAKOTLPVIYVKLYMQLFRSLA 180
        |||
Qy      181 YIHSFGICHRDIPQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFG 240
        |||
Db      181 YIHSFGICHRDIPQNLIDPDPAVLKLCDFGSAKOLVRGEPNVSYICSRYYRAPELIFG 240
        |||
Qy      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPREQIRENNPYTE 300
        |||
Db      241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPREQIRENNPYTE 300
        |||
Qy      301 FKFPQIAHPWTQVFRPRTPEAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
        |||
Db      301 FKFPQIAHPWTQVFRPRTPEAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
        |||
Qy      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394
        |||
Db      361 PNGRDTPALFNFPTTQELSSNPPLATILIPPHARI 394

```

RESULT 4

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US-09-916-109-1
; Sequence 1, Application US/09916109
; Patent No. US20020082408A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/09/916,109
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11

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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-09-916-109-1

Query Match 97.3%; Score 2024; DB 3; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 190
DB 121 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 180
QY 191 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 250
DB 181 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 240
QY 251 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 5
US-10-211-412A-1
Sequence 1, Application US/10211412A
Publication No. US2003007798A1
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacia, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: PP-15876, 004/200130, 524D1
CURRENT APPLICATION NUMBER: US/10/211, 412A
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-412A-1

Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 60

QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 190
DB 121 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 180
QY 191 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 250
DB 181 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 240
QY 251 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 6
US-10-278-759-7
Sequence 7, Application US/10278759
Publication No. US20030114382A1
GENERAL INFORMATION:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
FILE REFERENCE: S01237, 70020, US
CURRENT APPLICATION NUMBER: US/10/278, 759
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: US 60/350160
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/337905
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-278-759-7

Query Match 97.3%; Score 2024; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164; Indels 0; Gaps 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 70
DB 1 MSGRPTTSFAESCKPVOQPSAFSGSMKVS RDKDSKVTTVVATPGQGPDRPQEVSYTDTK 60
QY 71 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 130
DB 61 VINGSGFVVYQAKLCDSGELVAIKKVLQDKRFKRELIQIMRKLDHCNI VLRIFYSSG 120
QY 131 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 190
DB 121 EKKDEVYNTLVLDVPEVTVVAVAHYSRAKOTLPVIYKLYMYOLFRLSLAYHSFGICHR 180
QY 191 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 250
DB 181 DIKQONLLDPDPTAVLKLCDFGSAKQLVRGEPNVS YICSRYYRABELIFGATDYSIDV 240
QY 251 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 310
DB 241 WSACCVLAELLGQPIFPDGSVDQVLEIIVLGTPTREQIREMNPNTTEKFPQIKAH 300
QY 311 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPALALCSRLLEYTPPTARLTPLCAHSPFDELRDPNVKHPNGRDTPALF 360

Db 301 WTKVFRPTPEALALCSRLLETPPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 7

US-10-482-524-4
; Sequence 4, Application US/10482524
; Publication No. US20040261137A1
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham PLC
; APPLICANT: Holder: Julie C
; TITLE OF INVENTION: Models for Metabolic Disorders
; FILE REFERENCE: PG4458
; CURRENT APPLICATION NUMBER: US/10/482,524
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB 0115570.4
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: GB 0205604.2
; PRIOR FILING DATE: 2002-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-524-4

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDQSGSKYTTVATPGQSPDRPOEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDQSGSKYTTVATPGQSPDRPOEVSYTDTK 60
Qy 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRFFYSSG 130
Db 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRFFYSSG 120
Qy 131 EKDDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVTVKLYMQLPRLSLAYIHSFGICHR 190
Db 121 EKDDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVTVKLYMQLPRLSLAYIHSFGICHR 180
Qy 191 DIKPQNLDPDPTAVLKLCSGSAKOLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
Db 181 DIKPQNLDPDPTAVLKLCSGSAKOLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIRBMNPVTEKFPQIKAP 310
Db 241 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIRBMNPVTEKFPQIKAP 300
Qy 311 WTKVFRPTPEALALCSRLLETPPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEALALCSRLLETPPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 8

US-10-772-636-72
; Sequence 72, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21944, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014

; FILE REFERENCE: MPI03-01SP1RNMNMIM

; CURRENT APPLICATION NUMBER: US/10/772,636

; CURRENT FILING DATE: 2004-02-05

; PRIOR APPLICATION NUMBER: US 60/445,241

; PRIOR FILING DATE: 2003-02-05

; PRIOR APPLICATION NUMBER: US 60/448,389

; PRIOR FILING DATE: 2003-02-18

; PRIOR APPLICATION NUMBER: US 60/456,320

; PRIOR FILING DATE: 2003-03-20

; PRIOR APPLICATION NUMBER: US 60/460,279

; PRIOR FILING DATE: 2003-04-03

; PRIOR APPLICATION NUMBER: US 60/465,924

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: US 60/470,052

; PRIOR FILING DATE: 2003-05-13

; PRIOR APPLICATION NUMBER: US 60/498,106

; PRIOR FILING DATE: 2003-08-26

; PRIOR APPLICATION NUMBER: US 60/500,179

; PRIOR FILING DATE: 2003-09-04

; PRIOR APPLICATION NUMBER: US 60/502,909

; PRIOR FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: US 60/510,351

; PRIOR FILING DATE: 2003-10-10

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 72

; LENGTH: 420

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-772-636-72

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDQSGSKYTTVATPGQSPDRPOEVSYTDTK 70
Db 1 MSGRPRTTSPAESCKPVQQPSAFSGMKVSRDQSGSKYTTVATPGQSPDRPOEVSYTDTK 60
Qy 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRFFYSSG 130
Db 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIMRKLDHCNIVRLRFFYSSG 120
Qy 131 EKDDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVTVKLYMQLPRLSLAYIHSFGICHR 190
Db 121 EKDDEVYLNVLVDYVPEVTVRVARHYSRAKQTLPIVTVKLYMQLPRLSLAYIHSFGICHR 180
Qy 191 DIKPQNLDPDPTAVLKLCSGSAKOLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
Db 181 DIKPQNLDPDPTAVLKLCSGSAKOLVRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
Qy 251 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIRBMNPVTEKFPQIKAP 310
Db 241 WSAGCVLAELLGQPIFGDSDVDQVLEIKVLGTPTREQIRBMNPVTEKFPQIKAP 300
Qy 311 WTKVFRPTPEALALCSRLLETPPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPTPEALALCSRLLETPPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
Qy 371 NFTTOELSSNPPLATILIPPHARI 394
Db 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 9

US-10-689-461-1

Sequence 1, Application US/10689461
Publication No. US20050046511A1
GENERAL INFORMATION:
APPLICANT: Harrison, Stephen D.
APPLICANT: Hall, John A.
APPLICANT: Calderon-Cacela, Maria
APPLICANT: Zhong, Ziyang
APPLICANT: Pang, Eric Y.
APPLICANT: Colt, Doris G.
APPLICANT: Nguyen, Steve H.
APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/JP-15876.002/200130.524
CURRENT APPLICATION NUMBER: US/10/689,461
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US/10/211,412
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916,109
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-689-461-1

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2,6e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGSKTTVVATPGQGPDRQEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGSKTTVVATPGQGPDRQEVSYDTK 60
QY 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIRKLDHCNIIVLRFFYS5G 130
DB 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIRKLDHCNIIVLRFFYS5G 120
QY 131 EKQDEVYLVNLDVPEVTVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKQDEVYLVNLDVPEVTVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIRQNLILDPDVAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
DB 181 DIRQNLILDPDVAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
QY 251 WSACCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQOIRENNPNYTEKFPQIKANP 310
DB 241 WSACCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQOIRENNPNYTEKFPQIKANP 300
QY 311 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTQELSSNPPLATILIPPHARI 394
DB 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 10
US-10-840-060-257
Sequence 257, Application US/10840060
Publication No. US20050227243A1
GENERAL INFORMATION:
APPLICANT: Cyclacel Limited
APPLICANT: Deak, Peter
APPLICANT: Frenz, Lisa
APPLICANT: Glover, David
APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: 10069/2012
CURRENT APPLICATION NUMBER: US/10/840,060

CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: PCT/GB02/04780
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 0126506.5
PRIOR FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: GB 0128384.5
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: GB 0203185.4
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PatentIn version 3.1
SEQ ID NO 257
LENGTH: 420
TYPE: PRT
ORGANISM: Homo sapiens
US-10-840-060-257

Query Match 97.3%; Score 2024; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 2,6e-164;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGSKTTVVATPGQGPDRQEVSYDTK 70
DB 1 MSGRPRTTSFAESCKPVQPSAFSGMKVSRDKSGSKTTVVATPGQGPDRQEVSYDTK 60
QY 71 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIRKLDHCNIIVLRFFYS5G 130
DB 61 VINGSGFVVYQAKLCSGSELVAIKVLODKRFKRELOIRKLDHCNIIVLRFFYS5G 120
QY 131 EKQDEVYLVNLDVPEVTVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 190
DB 121 EKQDEVYLVNLDVPEVTVVARHYSRAKOTLPVIYVKLYMYOLFSLAYIHSFGICHR 180
QY 191 DIRQNLILDPDVAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 250
DB 181 DIRQNLILDPDVAVLKLCDFGSAKQVLRGEPNVSYICSRYYRABELIFGATDYTSIDV 240
QY 251 WSACCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQOIRENNPNYTEKFPQIKANP 310
DB 241 WSACCVLAELLGQPIFGDSGVQDLVEIIKVLGTPTRQOIRENNPNYTEKFPQIKANP 300
QY 311 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPTPEPEALALCSRLLEYTPPTARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTQELSSNPPLATILIPPHARI 394
DB 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 11
US-10-746-545-31
Sequence 31, Application US/10746545
Publication No. US20040171075A1
GENERAL INFORMATION:
APPLICANT: Deciphera Pharmaceuticals, Inc.
APPLICANT: Flynn, Daniel L
APPLICANT: Pecilio, Peter A
TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
FILE REFERENCE: 34475
CURRENT APPLICATION NUMBER: US/10/746,545
CURRENT FILING DATE: 2003-12-24
PRIOR APPLICATION NUMBER: US 60/437,487
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-746-545-31

Query Match 96.7%; Score 2013; DB 4; Length 414;

Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MSGRPRTTSPAESCKPVQOPSAFGSMKVS RDKDGSKVTTVATPGQGPDRPOEVS YTDTK 60

Qy 71 VINGSGGVVYQALCDSGELVAIKVLDQKRFKNRELQIMRKLDHCNIYLRARFFYS SG 130
Db 61 VINGSGGVVYQALCDSGELVAIKVLDQKRFKNRELQIMRKLDHCNIYLRARFFYS SG 120

Qy 131 EKDEVLNVLVDVPEPTVYVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVLNVLVDVPEPTVYVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKQNLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYSIDV 250
Db 121 EKDEVLNVLVDVPEPTVYVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 180

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 12
US-10-278-759-6
; Sequence 6, Application US/10278759
; Publication No. US20030114382A1
; GENERAL INFORMATION:
; APPLICANT: Malah, Kenneth
; TITLE OF INVENTION: Glycogen Synthase Kinase Function in Endothelial Cells
; FILE REFERENCE: S01237.70020.US
; CURRENT APPLICATION NUMBER: US/10/278, 759
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/350160
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/337905
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-278-759-6

Query Match 96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 300

Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

RESULT 13
US-10-135-255-1
; Sequence 1, Application US/10135255
; Publication No. US20030125332A1
; GENERAL INFORMATION:
; APPLICANT: TER HAAR, ERNST
; APPLICANT: GREEN, JEREMY
; APPLICANT: SWENSON, LOYORKA
; APPLICANT: ARNOST, MICHAEL J.
; TITLE OF INVENTION: INHIBITORS OF GSK-3 AND CRYSTAL STRUCTURES OF GSK-3B
; FILE REFERENCE: VPI/01-02
; CURRENT APPLICATION NUMBER: US/10/135,255
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/361,899
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/297,094
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/287,366
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-255-1

Query Match 96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 71 VINGSGGVVYQALCDSGELVAIKVLDQKRFKNRELQIMRKLDHCNIYLRARFFYS SG 130
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Qy 131 EKDEVLNVLVDVPEPTVYVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 190
Db 121 EKDEVLNVLVDVPEPTVYVARHYSRAKQTLPIYVVKLYMYQLFRSLAYIHSFGICHR 180

Qy 191 DIKQNLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYSIDV 250
Db 181 DIKQNLDPDPTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRABELIFGATDYSIDV 240

Qy 251 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 310
Db 241 WSAGCVLAELLGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPYTEKFPQIRAH 300

Qy 311 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 370
Db 301 WTKVFRPRTPEPAIALCSRLLEYTPARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360

Qy 371 NFTTQELSSNPPLATILIPPHARI 394
Db 361 NFTTQELSSNPPLATILIPPHARI 384

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RESULT 14
US-10-746-545-15
; Sequence 15, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphra Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-545-15

Query Match          96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 71 VINGSGFGVVYQAKLCDSGELVAIKVLDQKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 130
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QY 131 EKDQEVYLNVLVDVPEVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 190
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DB 241 WSACCVLAELLIGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
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DB 301 WTKVFRPRTPEBAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384

RESULT 15
US-10-746-545-18
; Sequence 18, Application US/10746545
; Publication No. US20040171075A1
; GENERAL INFORMATION:
; APPLICANT: Deciphra Pharmaceuticals, Inc.
; APPLICANT: Flynn, Daniel L
; APPLICANT: Pettilo, Peter A
; TITLE OF INVENTION: MODULATION OF PROTEIN FUNCTIONALITIES
; FILE REFERENCE: 34475
; CURRENT APPLICATION NUMBER: US/10/746,545
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/437,487
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 18
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-746-545-18

Query Match          96.7%; Score 2013; DB 4; Length 420;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 71 VINGSGFGVVYQAKLCDSGELVAIKVLDQKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 130
DB 61 VINGSGFGVVYQAKLCDSGELVAIKVLDQKRFKQRELIQMRKLDHCNIYRLRYFFYSSG 120
QY 131 EKDQEVYLNVLVDVPEVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 190
DB 121 EKDQEVYLNVLVDVPEVYRVARHYSRAKQTLPIYVKLYMYQLFRSLAYIHSFGICHR 180
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DB 181 DIKQNLILDDPTAVLKLCDFGSAKQLVRGEPNYSYICSRYYRABELIFGATDYSIDV 240
QY 251 WSACCVLAELLIGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPNTYEFKFPQIKAH 310
DB 241 WSACCVLAELLIGQPIFPDGSVDQVLEIIKVLGTPTRQIREMNPNTYEFKFPQIKAH 300
QY 311 WTKVFRPRTPEBAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALF 370
DB 301 WTKVFRPRTPEBAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NPTTOELSSNPPLATILIPPHARI 394
DB 361 NPTTOELSSNPPLATILIPPHARI 384
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Title: US-10-689-461-2
Perfect score: 2081
Sequence: 1 MEYMPMEGGMGSGRPTTSF.....OELSNPLATILIPPHARI 394

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Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2081	100.0	394	8 US-10-733-816-2	Sequence 2, Appl1
2	2024	97.3	420	8 US-10-733-816-1	Sequence 1, Appl1
3	2024	97.3	420	11 US-11-288-493-72	Sequence 72, Appl1
4	1996.5	95.9	433	9 US-10-770-726-65	Sequence 65, Appl1
5	1883.5	90.5	361	8 US-10-733-816-3	Sequence 3, Appl1
6	1609	77.3	447	8 US-10-733-816-5	Sequence 5, Appl1
7	1609	77.3	483	9 US-10-733-816-4	Sequence 4, Appl1
8	1609	77.3	483	9 US-10-451-375-12	Sequence 12, Appl1
9	1588	76.3	351	8 US-10-733-816-7	Sequence 7, Appl1
10	1588	76.3	387	8 US-10-733-816-6	Sequence 6, Appl1
11	1296	62.3	409	11 US-11-188-298-2916	Sequence 2916, Ap
12	1274	61.2	414	11 US-11-188-298-13961	Sequence 13961, A
13	1264	60.7	394	11 US-11-188-298-20391	Sequence 20391, A
14	1259	60.5	412	11 US-11-188-298-2343	Sequence 2343, Ap
15	1256	60.4	411	11 US-11-188-298-18419	Sequence 18419, A
16	1256	60.4	412	11 US-11-188-298-11847	Sequence 11847, A
17	1255.5	60.3	405	11 US-11-188-298-9056	Sequence 9056, Ap
18	1250	60.1	407	11 US-11-188-298-17827	Sequence 17827, Ap
19	1250	60.1	407	11 US-11-188-298-19883	Sequence 19883, A
20	1249	60.0	403	11 US-11-188-298-9267	Sequence 9267, Ap
21	1249	60.0	403	11 US-11-188-298-13637	Sequence 13637, A

22	1248.5	60.0	412	11 US-11-188-298-10609	Sequence 10609, A
23	1244	59.8	411	11 US-11-188-298-10624	Sequence 10624, A
24	1243.5	59.8	412	11 US-11-188-298-3285	Sequence 3285, Ap
25	1242.5	59.7	419	11 US-11-188-298-22443	Sequence 22443, A
26	1241	59.6	402	11 US-11-188-298-15003	Sequence 15003, A
27	1240.5	59.6	496	11 US-11-188-298-14293	Sequence 14293, A
28	1239	59.5	409	11 US-11-188-298-12421	Sequence 12421, A
29	1236.5	59.4	400	11 US-11-188-298-15000	Sequence 15000, A
30	1234.5	59.3	404	11 US-11-188-298-1871	Sequence 1871, Ap
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34	1231.5	59.2	397	11 US-11-188-298-5437	Sequence 5437, Ap
35	1230.5	59.1	403	11 US-11-188-298-21943	Sequence 21943, A
36	1228.5	59.0	403	11 US-11-188-298-1737	Sequence 1737, Ap
37	1226	58.9	411	11 US-11-188-298-1737	Sequence 1737, A
38	1226	58.9	468	11 US-11-188-298-14237	Sequence 14237, A
39	1225	58.9	414	11 US-11-188-298-17137	Sequence 17137, A
40	1222.5	58.7	394	11 US-11-188-298-2187	Sequence 2187, Ap
41	1221.5	58.7	401	11 US-11-188-298-11664	Sequence 11664, A
42	1220.5	58.6	341	11 US-11-188-298-18416	Sequence 18416, A
43	1218.5	58.6	421	11 US-11-188-298-7320	Sequence 7320, Ap
44	1208.5	58.1	420	11 US-11-188-298-10248	Sequence 10248, A
45	1199.5	57.6	468	11 US-11-188-298-17561	Sequence 17561, A

ALIGNMENTS

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RESULT 1
US-10-733-816-2
; Sequence 2, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT FILING DATE: US/10/733, 816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211, 412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916, 109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-2
Query Match      100.0%; Score 2081; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 3e-177;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEYMPMEGGMGSGRPTTSFAESCKPVQPSAFSGSMKVRSDKSKVTTVAATPGQGBDR 60
DB 1 MEYMPMEGGMGSGRPTTSFAESCKPVQPSAFSGSMKVRSDKSKVTTVAATPGQGBDR 60
QY 61 PQSVSYDTKYTGNGSGGVYQATLCSGSELVAIKKYLQDRFRKREIQIRKIDHCNIV 120
DB 61 PQSVSYDTKYTGNGSGGVYQATLCSGSELVAIKKYLQDRFRKREIQIRKIDHCNIV 120
QY 121 RLRFFSSGSGKEQVNLVLDVVPETVVRVAHYSRAKOTLPIVYVKLYMYOLFSLA 180
DB 121 RLRFFSSGSGKEQVNLVLDVVPETVVRVAHYSRAKOTLPIVYVKLYMYOLFSLA 180
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```
QY 181 YHSFGI:CHRDIKPONLLDPDTAVLKUCDFGSAKOLVRGEPNYSICRYRABELIFG 240
DB 181 YHSFGI:CHRDIKPONLLDPDTAVLKUCDFGSAKOLVRGEPNYSICRYRABELIFG 240
QY 241 ATDYTSSIDVWSAGCVLAELLGGPIFPDGSVDQVLEIIKVLGTPTRREQIRENNPNYTE 300
DB 241 ATDYTSSIDVWSAGCVLAELLGGPIFPDGSVDQVLEIIKVLGTPTRREQIRENNPNYTE 300
QY 301 FKFPQIRAHPTKXFRPRTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
DB 301 FKFPQIRAHPTKXFRPRTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKH 360
QY 361 PNGRDTPALFNTTOELSSNPPLATILIPPHARI 394
DB 361 PNGRDTPALFNTTOELSSNPPLATILIPPHARI 394

RESULT 2
US-10-733-816-1
; Sequence 1, Application US/10733816
; Publication No. US20060088932M1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacela, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876_002/200130_524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-1

Query Match 97.3%; Score 2024; DB 8; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 301 WTKVFRPRTPEPAIALCSRLLEYPTARLTPLBACAHSPFDELDPNVKHPNGRDTPALF 360
QY 371 NFTTOELSSNPPLATILIPPHARI 394
DB 361 NFTTOELSSNPPLATILIPPHARI 384

RESULT 3
US-11-288-493-72
; Sequence 72, Application US/11288493
; Publication No. US20060078947A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014
; FILE REFERENCE: MPI03-015P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/11/288,493
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US/10/772,636
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US 60/445,241
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,389
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/456,320
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/460,279
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/465,924
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/470,052
; PRIOR FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: US 60/498,106
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/500,179
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/502,909
; PRIOR FILING DATE: 2003-09-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-288-493-72

Query Match 97.3%; Score 2024; DB 11; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.6e-166;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 181 DIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSICSRYYRAPELFGATDNTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTEFKFPOIKAH 310
Db 241 WSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTEFKFPOIKAH 300
Qy 311 WTKVRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPGRDTPALF 370
Db 301 WTKVRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVKHPGRDTPALF 360
Qy 371 NFTQELSSNPPLATILIPPHARI 394
Db 361 NFTQELSSNPPLATILIPPHARI 384

RESULT 4
US-10-770-726-65
; Sequence 65, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM:01079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-65

Query Match 95.9%; Score 1996.5; DB 9; Length 433;
Best Local Similarity 96.5%; Pred. No. 6.3e-164;
Matches 383; Conservative 0; Mismatches 1; Indels 13; Gaps 1;

Qy 11 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKGSKTTTVAATPGQGPDRPQEVSYDTK 70
Db 1 MSGRRTTSPAESCKPVOQPSAFSGMKVSRDKGSKTTTVAATPGQGPDRPQEVSYDTK 60
Qy 71 VINGSGFVVYQAKLCDSGELVAIKVLDKRFKNRELQIMRKLDHCNIIVLRFPFSSG 130
Db 61 VINGSGFVVYQAKLCDSGELVAIKVLDKRFKNRELQIMRKLDHCNIIVLRFPFSSG 120
Qy 131 EKQDEVYINLVLDYVPEVTVYRAHYSAKQTLPIYIVKLYMYQLFRSLAYTHSGICHR 190
Db 121 EKQDEVYINLVLDYVPEVTVYRAHYSAKQTLPIYIVKLYMYQLFRSLAYTHSGICHR 180
Qy 191 DIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSICSRYYRAPELFGATDNTSSIDV 250
Db 181 DIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSICSRYYRAPELFGATDNTSSIDV 240
Qy 251 WSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTEFKFPOIKAH 310
Db 241 WSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTEFKFPOIKAH 300
Qy 311 WTK-----VRRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPN 357
Db 301 WTKSSSGTGHFTSGVVRPRPRPPPAIALCSRLLEYTPARLTPLACAHSPFDELDPN 360
Qy 358 VKHPNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 361 VKLPNGRDTPALFNTTQELSSNPPLATILIPPHARI 397

RESULT 5
US-10-733-816-3
; Sequence 3, Application US/10733816
; Publication No. US20060088932A1

; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-3

Query Match 90.5%; Score 1883.5; DB 8; Length 361;
Best Local Similarity 91.6%; Pred. No. 2.6e-154;
Matches 361; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

Qy 1 MEYPMEGGSGRPRRTTSPAESCKPVOQPSAFSGMKVSRDKGSKTTTVAATPGQGPDR 60
Db 1 MEYPMEGGSG-----GSKTTTVAATPGQGPDR 27
Qy 61 POEVSYDTKVIINGSGFVVYQAKLCDSGELVAIKVLDKRFKNRELQIMRKLDHCNIIV 120
Db 28 POEVSYDTKVIINGSGFVVYQAKLCDSGELVAIKVLDKRFKNRELQIMRKLDHCNIIV 87
Qy 121 RLRFPFSSGKQDEVYINLVLDYVPEVTVYRAHYSAKQTLPIYIVKLYMYQLFRSLA 180
Db 88 RLRFPFSSGKQDEVYINLVLDYVPEVTVYRAHYSAKQTLPIYIVKLYMYQLFRSLA 147
Qy 181 YIHSFGICHRDIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSICSRYYRAPELFG 240
Db 148 YIHSFGICHRDIKPNLLDPTAVLKLCDFGSAKQVLRGEPNVSICSRYYRAPELFG 207
Qy 241 ATDNTSSIDVWSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTE 300
Db 208 ATDNTSSIDVWSAGCVLAELLGQPIFFGDSGVQDLVEIIKVLTGPTREQIREMNPNTTE 267
Qy 301 FKFPOIKAHPTKVFRRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVK 360
Db 268 FKFPOIKAHPTKVFRRPRTPEPAIALCSRLLEYTPARLTPLACAHSPFDELDPNVK 327
Qy 361 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 394
Db 328 PNGRDTPALFNTTQELSSNPPLATILIPPHARI 361

RESULT 6
US-10-733-816-5
; Sequence 5, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524

```

CURRENT APPLICATION NUMBER: US/10/733, 816
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US/10/211, 412
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916, 109
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
US-10-733-816-5

Query Match      77.3%; Score 1609; DB 8; Length 447;
Best Local Similarity 80.6%; Pred. No. 1,4e-130;
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3

QY      8 GGGMSGRRT-TSFAESCKPVQGPAPFSMKVSRDQSKYTTVATPGQGPDRPOEVS 66
        ||||| ||||| ||||| :||| ||||| ||||| ||||| |||||
DB      73 GGGSGGGGAGTSPFP-----GVKLR--DSGKVTVAATGQGERSQEYAY 119

QY      67 TDTKYINGSGFVYQAKLCDSGELVAIKVQLQDRFPKNRELQIRKLDHCNIVRLRYFF 126
        ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB      120 TDIKVIKNGSGCVYQARLAETRELVAIKVQLQDRFPKNRELQIRKLDHCNIVRLRYFF 179

QY      127 YSSGEKDEVYLVLDVYPETVYVAHYSRAKOTLPVIYKLYMYQLFRSLAYHSFG 186
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      180 YSSGEKDELYLVLDVYEPETVYVAHFTYAKTLPILYKVMYQLFRSLAYHSQG 239

QY      187 ICHDIDIKQNLDPDVTAVLKCDGSKAKQVREGSPNYSICSRYYRABELLFGATDYS 246
        :|||: ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||:
DB      240 VCHRIKQNLVDDVTIVLKCDGSKAKQVREGSPNYSICSRYYRABELLFGATDYS 299

QY      247 SIDWSACCVLAELLQGPPIFGDSGVQLVEIIVKLGTPTEQIREMNPYTEKFPQI 306
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      300 SIDWSACCVLAELLQGPPIFGDSGVQLVEIIVKLGTPTEQIREMNPYTEKFPQI 359

QY      307 KAHPTKVFPRPTPEPAIALCSRLLEYTPARLTPLEACAHSPDELDPNVKHPNGSDT 366
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      360 KAHPTKVFKSRTPEPAIALCSRLLEYTPSRSLPLEACAHSPDELCLGTQLPNNRPL 419

QY      367 PALPFTTQELSSNPPLATILIPHLAR 393
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      420 PPLFNFSAGELSIQSLNAILIPHLR 446
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-733-816-4
; Sequence 4, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacile, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Pang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
TITLE OF INVENTION: GSK3 POLYPEPTIDES
FILE REFERENCE: 59516-162/P-15876, 002/200130, 524
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US/10/733, 816
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US09/916, 109
PRIOR FILING DATE: 2001-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT

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Query Match	77.3%; Score 1609; DB 8; Length 483;
Beat Local Similarity 80.6%; Pred. No. 1,66-130;	
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3	
QY	8 GGGMSGRPR-TSPAESCQPVQGPSAFGSMKVSFKDQSKYTTVAVATPGQSDPRQEVSY 66
DB	73 GGGSGGGAGACTSPPP-----GVKLGR--DSGKVTIVATLGGQEPKSEQEYAV 119
QY	67 TDTKVIINGSGFVGYOAKLCDSGELVAIKYLDQKRFKNRELQIMRKLDHCNIYRLRYFF 126
DB	120 TDIKVIINGSGFVGYOARLATTRELVAIKYLDQKRFKNRELQIMRKLDHCNIYRLRYFF 179
QY	127 YSSGEKDEYVNLVLDVPEPTVYRVARHYSRAKQTLPIVIYKLYMYQLFSLAYIHSFG 186
DB	180 YSSGEKDEYVNLVLEVPETVYRVARHFTAKLTILYKVKYMYQLFSLAYIHSQG 239
QY	187 ICHADIKQNLILDPDTAVLKLCDFGSKKOLVRGPNVSYICSRYYRAPELIFGATDVT 246
DB	240 VCHADIKQNLILVDPDTAVLKLCDFGSKKOLVRGPNVSYICSRYYRAPELIFGATDVT 299
QY	247 SIDWSAGCVLAELLGQPIFGSGVDQVEIIKVLGTPPREQIREKNPNYTEKFPQI 306
DB	300 SIDWSAGCVLAELLGQPIFGSGVDQVEIIKVLGTPPREQIREKNPNYTEKFPQI 359
QY	307 KAHFWTKVFRPTPEPAIALCSRLLEYTPTRALTPLECAHSPFDELDPVYKHNGRDT 366
DB	360 KAHFWTKVFRPTPEPAIALCSRLLEYTPSSRLSPLECAHSPFDELCLGQLPNNRPL 419
QY	367 PALNFTTQELSSNPPLATILIPPHAR 393
DB	420 PPLNFTSAGELSIQPSLNAIILIPHLR 446
RESULT 8	
US-10-451-375-12	
; Sequence 12, Application US/10451375	
; Publication No. US20050261482A1	
; GENERAL INFORMATION:	
; APPLICANT: Bayer AG	
; TITLE OF INVENTION: REGULATION OF HUMAN SERINE-THREONINE PROTEIN KINASE	
; FILE REFERENCE: LIO264 Foreign Countries	
; CURRENT APPLICATION NUMBER: US/10/451,375	
; CURRENT FILING DATE: 2003-07-02	
; PRIOR APPLICATION NUMBER: US 60/259,215	
; PRIOR FILING DATE: 2001-01-03	
; PRIOR APPLICATION NUMBER: US 60/306,468	
; PRIOR FILING DATE: 2001-07-20	
; PRIOR APPLICATION NUMBER: US 60/308,098	
; PRIOR FILING DATE: 2001-07-30	
; NUMBER OF SEQ ID NOS: 14	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 12	
; LENGTH: 483	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-10-451-375-12	
Query Match	77.3%; Score 1609; DB 9; Length 483;
Beat Local Similarity 80.6%; Pred. No. 1,66-130;	
Matches 312; Conservative 24; Mismatches 37; Indels 14; Gaps 3	
QY	8 GGGMSGRPR-TSPAESCQPVQGPSAFGSMKVSFKDQSKYTTVAVATPGQSDPRQEVSY 66
DB	73 GGGSGGGAGACTSPPP-----GVKLGR--DSGKVTIVATLGGQEPKSEQEYAV 119
QY	67 TDTVIINGSGFVGYOAKLCDSGELVAIKYLDQKRFKNRELQIMRKLDHCNIYRLRYFF 126
DB	120 TDIKVIINGSGFVGYOARLATTRELVAIKYLDQKRFKNRELQIMRKLDHCNIYRLRYFF 179
QY	127 YSSGEKDEYVNLVLDVPEPTVYRVARHYSRAKQTLPIVIYKLYMYQLFSLAYIHSFG 186

```
Db 180 YSSGKQKQELVLTAVLEVPETVVAHFTKAKLTITILYKVMYQVLFRLAYIHSG 239
Qy 187 ICHRDIKQNLDDPTAVLKCDGSAKQVREGPNVSYICSRYYRAPELIFGATDYS 246
Db 240 VCHRIKQNLVDPDTAVLKCDGSAKQVREGPNVSYICSRYYRAPELIFGATDYS 299
Qy 247 SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGTPPREOIRENNPNTFEKFPQI 306
Db 300 SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGTPPREOIRENNPNTFEKFPQI 359
Qy 307 KAHPTKVFRRPTPEALALCSRLLEYTPTAALPLAECASFDELDPNVKGHNGRDT 366
Db 360 KAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEKCAHSFDELDGQLPNNRPL 419
Qy 367 PALFTTQELSSNPPLATILIPPHAR 393
Db 420 PPLFNFSAGELSIQPSLNAIILIPPHLR 446
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RESULT 9

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US-10-733-816-7
; Sequence 7, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-7
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```
Query Match 76.3%; Score 1588; DB 8; Length 351;
Best Local Similarity 86.2%; Pred. No. 6.7e-129;
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;

Qy 46 KTTTVAATPGGPRPOBVSYTDTKVIGNSFGVYVQAKLCDSGELVAIKKVLQDKRKN 105
Db 3 KTTTVAATLGGPSPQSEVATYTDIKVIGNSFGVYVQARLAEATRELVAIKKVLQDKRKN 62
Qy 106 RELQIMRKLCHCNVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAARHSAKQTLPIV 165
Db 63 RELQIMRKLCHCNVRLRYFFYSSEKKDEYVNLVLEVEPYRYRVAARHSAKQTLPI 122
Qy 166 IYKLVYVQVLFRLSLAYIHSGVCHRDIKPQNLVDPDTAVLKCDGSAKQVREGPNV 225
Db 123 LYKLVYVQVLFRLSLAYIHSGVCHRDIKPQNLVDPDTAVLKCDGSAKQVREGPNV 182
Qy 226 YICSRYYRAPELIFGATDYS SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGT 285
Db 183 YICSRYYRAPELIFGATDYS SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGT 242
Qy 286 PTRQIREMNPNTYEFKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPTAALPLAEC 345
Db 243 PTRQIREMNPNTYEFKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEK 302
```

```
Qy 346 AHSPFDELDPNVKGHNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 303 AHSPFDELDRCIGTQLPNNRPLPPLFNFSAGELSIQPSLNAIILIPPHLR 350
```

RESULT 10

```
US-10-733-816-6
; Sequence 6, Application US/10733816
; Publication No. US20060088932A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Stephen D.
; APPLICANT: Hall, John A.
; APPLICANT: Calderon-Cacia, Maria
; APPLICANT: Zhong, Ziyang
; APPLICANT: Fang, Eric Y.
; APPLICANT: Colt, Doris G.
; APPLICANT: Nguyen, Steve H.
; APPLICANT: Medina-Selby, Angelica
; TITLE OF INVENTION: GSK3 POLYPEPTIDES
; FILE REFERENCE: 59516-162/PP-15876.002/200130.524
; CURRENT APPLICATION NUMBER: US/10/733,816
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/10/211,412
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US09/916,109
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-816-6
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```
Query Match 76.3%; Score 1588; DB 8; Length 387;
Best Local Similarity 86.2%; Pred. No. 7.6e-129;
Matches 300; Conservative 22; Mismatches 26; Indels 0; Gaps 0;
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Qy 46 KTTTVAATPGGPRPOBVSYTDTKVIGNSFGVYVQAKLCDSGELVAIKKVLQDKRKN 105
Db 3 KTTTVAATLGGPSPQSEVATYTDIKVIGNSFGVYVQARLAEATRELVAIKKVLQDKRKN 62
Qy 106 RELQIMRKLCHCNVRLRYFFYSSEKKDEYVNLVLDYVETVYRVAARHSAKQTLPIV 165
Db 63 RELQIMRKLCHCNVRLRYFFYSSEKKDEYVNLVLEVEPYRYRVAARHSAKQTLPI 122
Qy 166 IYKLVYVQVLFRLSLAYIHSGVCHRDIKPQNLVDPDTAVLKCDGSAKQVREGPNV 225
Db 123 LYKLVYVQVLFRLSLAYIHSGVCHRDIKPQNLVDPDTAVLKCDGSAKQVREGPNV 182
Qy 226 YICSRYYRAPELIFGATDYS SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGT 285
Db 183 YICSRYYRAPELIFGATDYS SIDWSAGCVLAELLGGPIFGDSGVQVLEIIKVLGT 242
Qy 286 PTRQIREMNPNTYEFKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPTAALPLAEC 345
Db 243 PTRQIREMNPNTYEFKFPQIKAHPTKVFRRPTPEALALCSRLLEYTPSSLSLEK 302
Qy 346 AHSPFDELDPNVKGHNGRDTPALFNTTQELSSNPPLATILIPPHAR 393
Db 303 AHSPFDELDRCIGTQLPNNRPLPPLFNFSAGELSIQPSLNAIILIPPHLR 350
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RESULT 11

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US-11-188-298-2916
; Sequence 2916, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
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; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2916
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Petunia x hybrida
US-11-188-298-2916

Query Match      62.3%; Score 1296; DB 11; Length 409;
Best Local Similarity 62.3%; Pred. No. 1.1e-103;
Matches 254; Conservative 49; Mismatches 75; Indels 30; Gaps 7;

Qy 4 MPMGGGSGRPRRTSFASCKPVOQPSAFSGMKVSRDK-----DSK----- 46
Db 6 MPMGSG---GKRRIDAMLV---KLPEINEMKIRDDKAEKEMBAVAVDNGTEKGIIT 57

Qy 47 VTTVAATPGGPDPRPOBVSYTDITKVIKNGSFGVYVYQAKLDSGELVAIKVYLQDPRFNR 106
Db 58 VTTI---GKKGGEPRQITISWAERVGGSGFVQAKLETGETVAIKVYLQDPRFNR 114

Qy 107 ELQIMRKLDHCNIVRLKRYFFSSGKKDEVTINLVLYVPEYTVRVVAHYSRAKQTLFVI 166
Db 115 ELQITRLLDHNNVALRHCFPSTTE-KDELYLINLVLEVPETVYRVLRHYSKAKQOMPMI 173

Qy 167 YVKLYMYQLPFRSLAYIHSFGICHRDIKQNLILDPDTAVLKLCPGSAKQLVGEPNVSY 226
Db 174 YVKLYTYQIFRALYIHGIGVCHRDIKQNLVNPHTQQLKCDPGSAKVLVKEPNISY 233

Qy 227 ICSRYVAPBELIFGATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTP 286
Db 234 ICSRYVAPBELIFGATEYTFALDIWSVGCVALLELLGQPLPGSGVQDLVEIIKVLGTP 293

Qy 287 TREQIRENNPVYTERKFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCA 346
Db 294 TREIRKSNPNVYTERKFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCA 353

Qy 347 HSFPDELRDNPVKHNPGRDTPALFNFTQEL-SSNPPLATILIPPHAR 393
Db 354 HTPDELRLDPKTRILPNGRPLPPLFNFRPQELKGSADLLNLKILPEHAK 401

RESULT 12
US-11-188-298-13961
; Sequence 13961, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13961
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-188-298-13961

Query Match      61.2%; Score 1274; DB 11; Length 414;
Best Local Similarity 60.8%; Pred. No. 8.6e-102;
Matches 239; Conservative 63; Mismatches 81; Indels 10; Gaps 4;

Qy 8 GGGGSG-----RRTTISFASCKPVOQPSAFSGMKVSRDQSGSKVTTVATPGGPDPR 61
Db 12 GGGGAADPMQVQGRSAAAAAVALPAGGKGSALMESGDPVTGHIISTTIG--GKNEBP 69

Qy 62 QEVSYTTTKVINGSGFVYVYQAKLDSGELVAIKVYLQDPRFNR 121
Db 70 RTISYMERVVGTSFGIVFQAKLETGETVAIKVYLQDPRFNR 129

; Sequence 2343, Application US/11188298
; Publication No. US20060075522A1

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Qy 122 LRYFFYSGGEKDEVTINLVLYVPEYTVRVVAHYSRAKQTLFVIYVKLYMYQLFRSLAY 181
Db 130 LKHCFFST-ISRDELFLNLMVEFVPSLVVLKHSNMNRMPLIYVKLYMYQLFRSLAY 188

Qy 182 IHSF-GICHRDIKQNLILDPDTAVLKLCPGSAKQLVGEPNVSYICSYRYAPBELIFG 240
Db 189 IHTVPGVCHRDVYQNLVLVPLTHQVKICDPSGAKMLVKEGANISYICSYRYAPBELIFG 248

Qy 241 ATDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPPREQIRENNPVYTE 300
Db 249 ATDYTSIDVWSAGCVLAELLGQPLPGSADVQDLVEIIKVLGTPPREIRMMNPVYTE 308

Qy 301 FKFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCAHSFPDELRLDPNVKH 360
Db 309 FRFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCAHSFPDELRLDPNVKH 368

Qy 361 PNGRDPALFNFTQELSSNPPLATILIPPHAR 393
Db 369 PNGRFPPLFNFKQELANISPELINRLIPEHAR 401

RESULT 13
US-11-188-298-20391
; Sequence 20391, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 20391
; LENGTH: 394
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-20391

Query Match      60.7%; Score 1264; DB 11; Length 394;
Best Local Similarity 70.8%; Pred. No. 5.8e-101;
Matches 240; Conservative 41; Mismatches 50; Indels 8; Gaps 3;

Qy 62 QEVSYTTTKVINGSGFVYVYQAKLDSGELVAIKVYLQDPRFNRQIRENNPVYTER 121
Db 31 KEIQYSGCKIVGSGFVYVYQAKLDSGELVAIKVYLQDPRFNRQIRENNPVYTER 90

Qy 122 LRYFFYSGGEKDEVTINLVLYVPEYTVRVVAHYSRAKQTLFVIYVKLYMYQLFRSLAY 181
Db 91 LKAFYNSNGRQDEVTINLVLYVPEYTVRVVAHYSRAKQTLFVIYVKLYMYQLFRSLAY 150

Qy 182 IHSF-GICHRDIKQNLILDPDTAVLKLCPGSAKQLVGEPNVSYICSYRYAPBELIFG 241
Db 151 IHSFGICHRDIKQNLILDPDTAVLKLCPGSAKQLVGEPNVSYICSYRYAPBELIFG 210

Qy 242 TDYTSIDVWSAGCVLAELLGQPIFGDSGVQDLVEIIKVLGTPPREQIRENNPVYTE 301
Db 211 TNYTTKIDVWSTCVNAEMLGQPLPGSGIDQDLVEIIKVLGTPPREQIRENNPVYTE 270

Qy 302 KFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCAHSFPDELRLDPNVK-- 359
Db 271 KFPQIKAHMPTKVFRRPTPEALCSRLLEYTPTRALPPLCAHSFPDELRLDPNVK 329

Qy 360 ---HPNG--RDTPALFNFTQELSSNPPLATILIPPHAR 393
Db 330 DSRHPNGAARDLPLNLFDSRHELSIAPSMNSRLVPPHRS 368

RESULT 14
US-11-188-298-2343
; Sequence 2343, Application US/11188298
; Publication No. US20060075522A1

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; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; PRIOR FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 2343
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Zea mays
US-11-188-298-2343

Query Match      60.5%; Score 1259; DB 11; Length 412;
Best Local Similarity 59.5%; Pred. No. 1.7e-100;
Matches 244; Conservative 62; Mismatches 76; Indels 28; Gaps 8;

Qy 1 MEYMEGGGMSGRRTTSFAESCKPVQ-----QPSAGSMKVSRDK-----DGSKVT 48
Db 1 MAAMP---GGAHG-----AGADPMOVDPPLPPAAGTAHAPADAKHAGSMIEGSDPV 50

Qy 49 T--VVAATP--GQGPDPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFX 104
Db 51 TGHISTITGGKNGEPKKTISTIMARVVGTSFGIVPQAKCLETGETVAIKKVLQDKRFX 110

Qy 105 NRELIQMKLDHCNIVRLRYFFYSSEKKEDEVYLVLDVYBETVYRVARHYSRAKQTLR 164
Db 111 NRELQIMSMDBHCNVVSLKHCFFSF--TSRDELFLVMEFVESLYRVLKHYSNNQRMF 169

Qy 165 VTYVLTVMYQLPRLSLAYIHSF-GICHRDIKPNLLDPTAVLKLCDFSAGAKQVLRGEPN 223
Db 170 LIYVLTYYQIFRGALAYHTVPGVCHRDVCPQNLVDPQLTHQVKICDFGSAMLVKGEAN 229

Qy 224 VSYICSRYYRAPELIFGATDYTSIDVWSAGCVLAELLLGQPIFPDGSVDQVLEIIRKL 283
Db 230 ISYICSRYYRAPELIFGATEYTSIDVWSAGCVLAELLLGQPLFPGESVDQVLEIIRKL 289

Qy 284 GTPTRQIRENNPNYTERFKFPQIKAPMTKVFRPRTPEPAIALCSRLLEYTPARLTPLE 343
Db 290 GTPTRBEIRCMNPNTYTERFRPQIKAPMHKIFHKMPPEAIDLASRLLOYSPNLRCTALE 349

Qy 344 ACAHSFPELADPNVKHNGRDTPLFNFPTQELSSNPPLATILIPPHAR 393
Db 350 ACAHFFDELREPHARLPNGRFPPLFNFQKELANASPELINRLIPDHAR 399

RESULT 15
US-11-188-298-18419
; Sequence 18419, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; PRIOR FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18419
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Medicago sativa
US-11-188-298-18419

Query Match      60.4%; Score 1256; DB 11; Length 411;
Best Local Similarity 61.2%; Pred. No. 3e-100;
Matches 248; Conservative 55; Mismatches 82; Indels 20; Gaps 8;

Qy 6 MEGGMSGRPRTTSFAESCKPV---QPSAGSMKVSRDK-----DGSKVT---VV 51
Db 6 MEGGMSGRPRTTSFAESCKPV---QPSAGSMKVSRDK-----DGSKVT---VV 51
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Db 1 MASGVA--PASGFIDKNASSVGEKLPENMDMKIRDDKEMEATYIVDNGTGTGHIIV 58
Qy 52 ATPGGPRP--QBSVYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQDKRFXRLQI 110
Db 59 TTIGKNGQPKQTISTYMERVVGHSFGVVPQAKCLETGETVAIKKVLQDKRFXRLQI 118
Qy 111 MRKLDHCNIVRLRYFFYSSEKKEDEVYLVLDVYBETVYRVARHYSRAKQTLRPIYVYL 170
Db 119 MRLDHPNVSLKQCFFSFSTE--KDELYLVNLEIVPEVSVKVIHRYHKNQRMFPIYVL 177
Qy 171 YMYQLFRSLAYIH-SFGICHRDIKPNLLDPTAVLKLCDFSAGAKQVLRGEPNVSYICS 229
Db 178 YSYQCRALAYIHSIGVCHNDIKPNLLVMPHTHQLKICDFGSAKVLVKGEPNISYICS 237
Qy 230 RYRAPPELIFGATDYTSIDVWSAGCVLAELLLGQPIFPDGSVDQVLEIIRKLGTPTRE 289
Db 238 RYRAPPELIFGATEYTSIDVWSAGCVLELLGQPLFPGESVDQVLEIIRKLGTPTRE 297
Qy 290 QIRENNPNYTERFKFPQIKAPMTKVFRPRTPEPAIALCSRLLEYTPARLTPLEACAHSF 349
Db 298 EIKCMNPYTERFKFPQIKAPMHKIFHKMPPEAVDLVSRLLQYSPNLRCTALEALVHPF 357
Qy 350 FDELADPNVKHNGRDTPLFNFPTQELSSNP-PLATILIPPHAR 393
Db 358 YDVPADPWTRLPNGRFLPPLFNFKNBELKGVPAEWLVLTVEPPHAR 402

Search completed: May 16, 2006, 15:25:20
Job time : 29 secs
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